

FIG. 1A

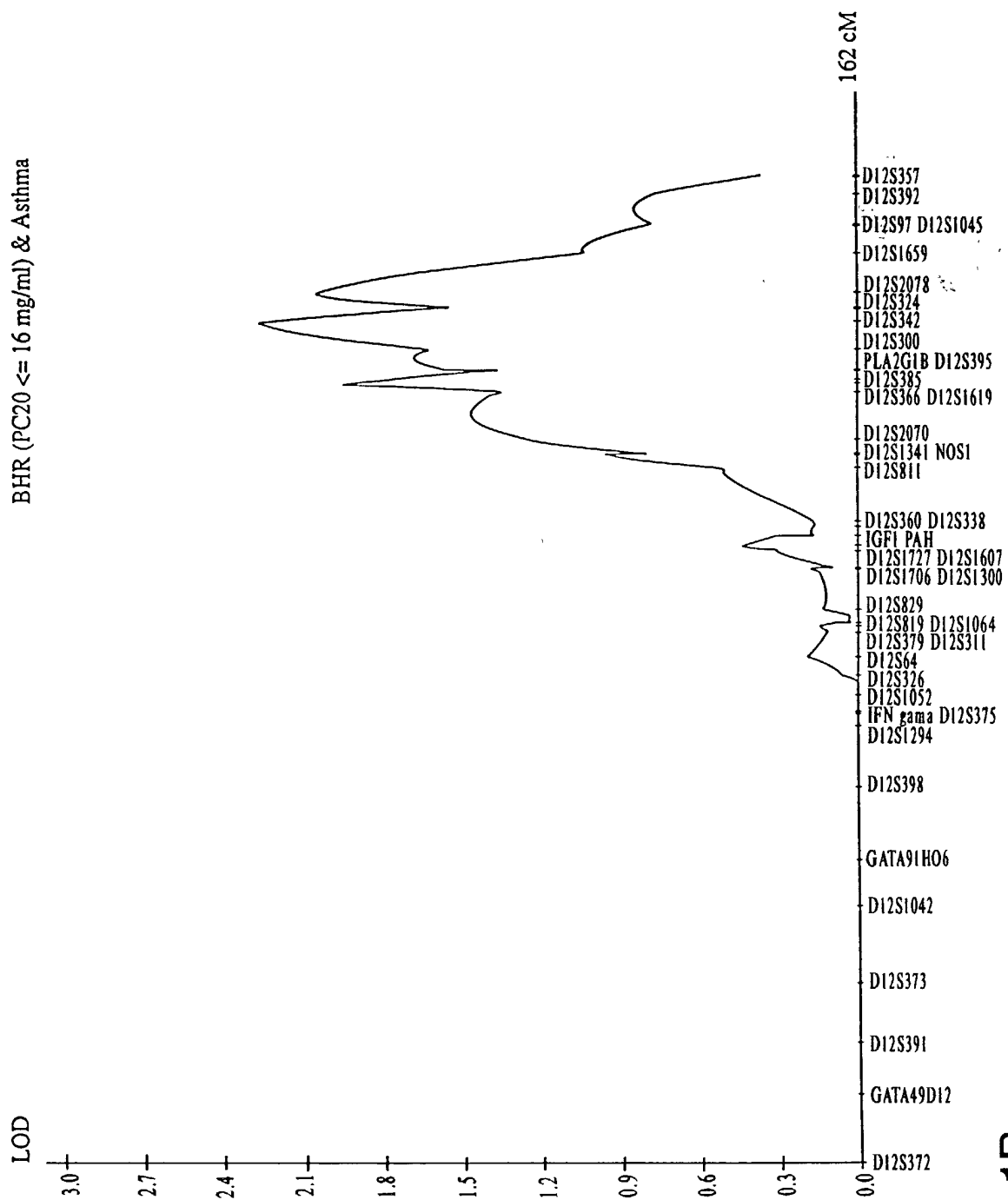


FIG. 1B

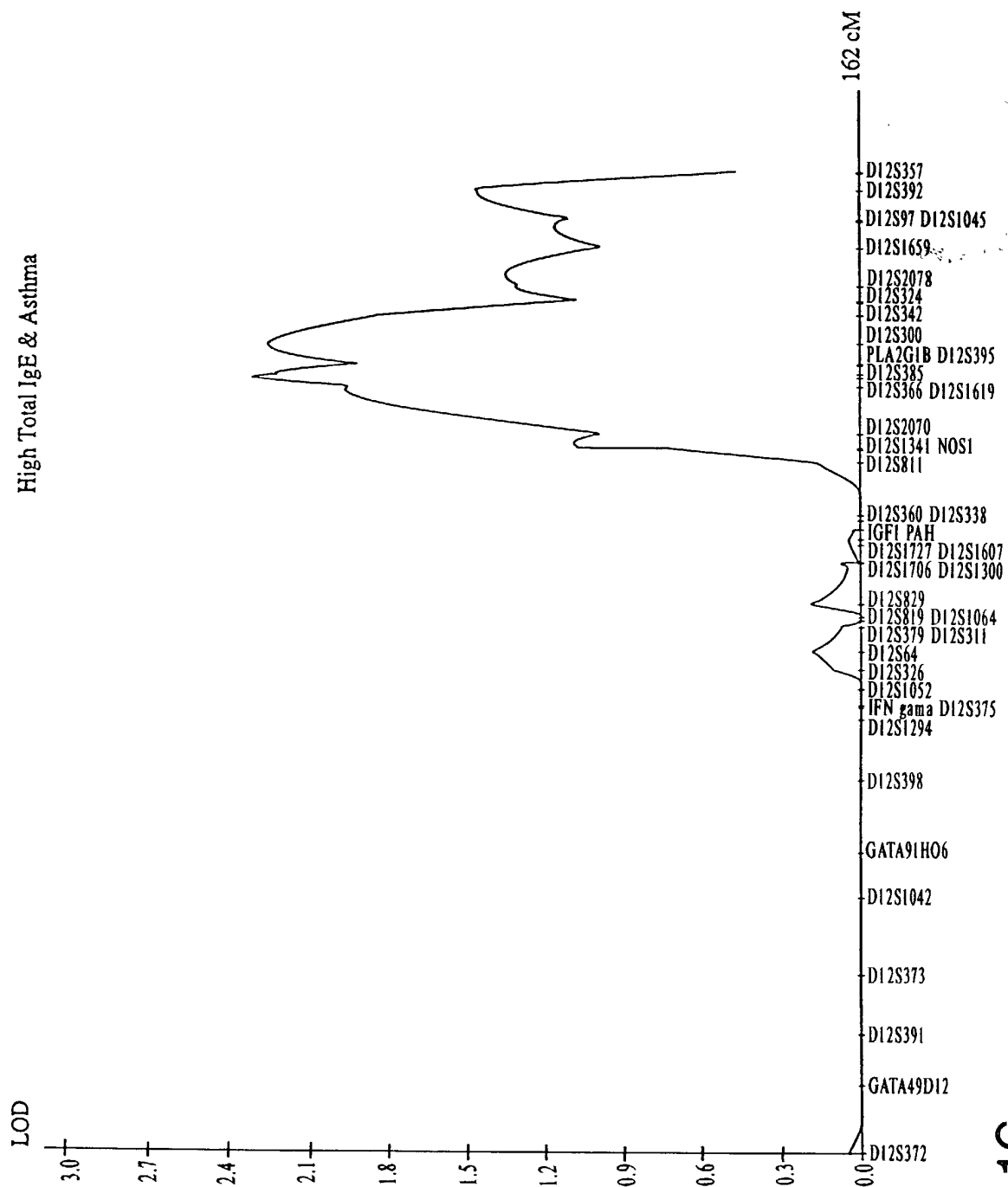


FIG. 1C

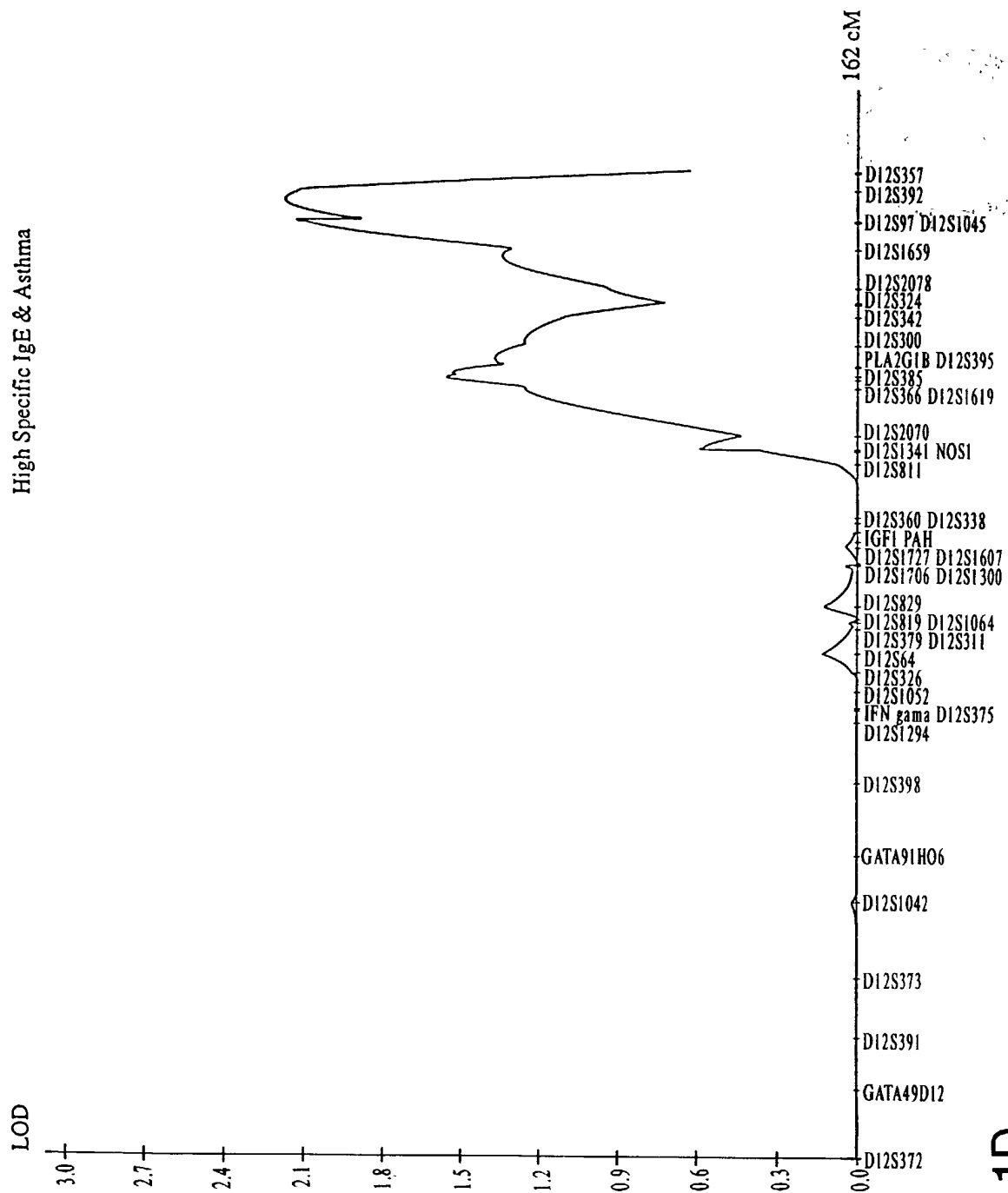
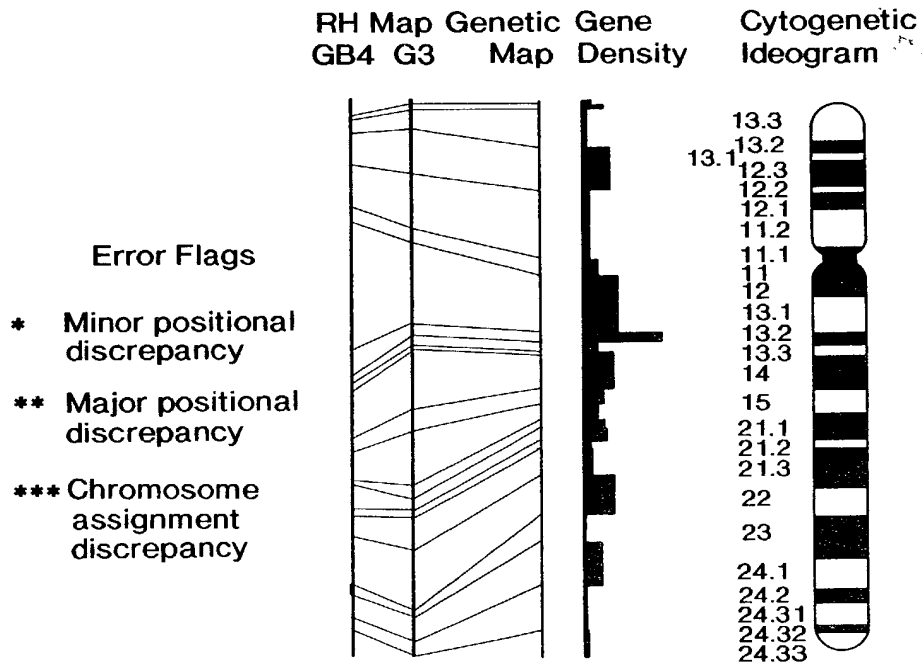


FIG. 1D

Chromosome 12: D12S79-D12S366



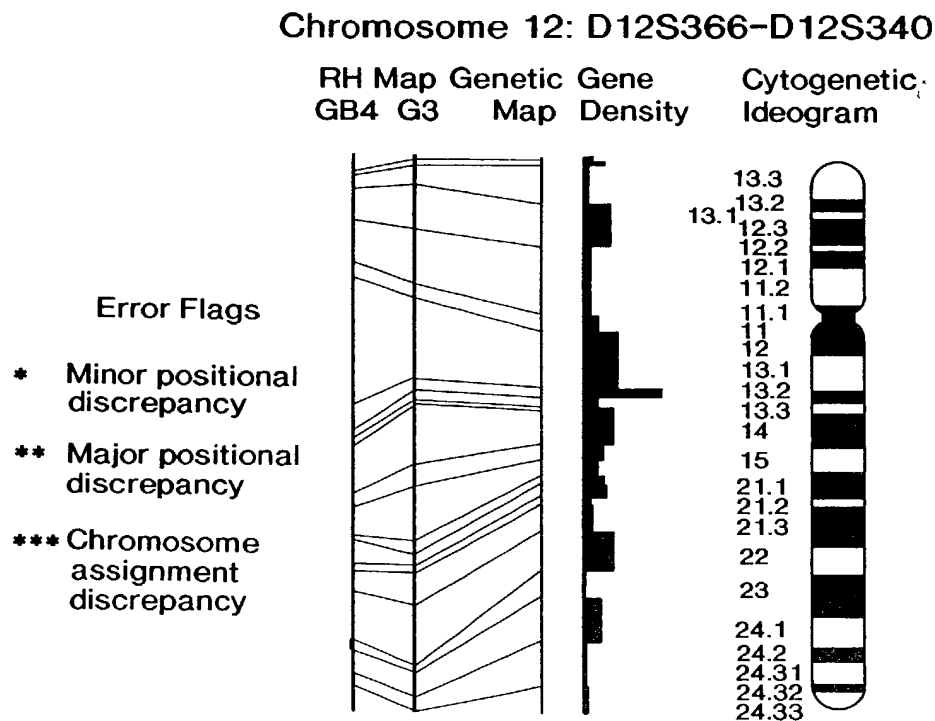
About This Interval

Top of interval:	D12S79 (126.1 cM)
Bottom of interval:	D12S366 (133.8 cM)
Genetic size of bin:	8 cM
Physical size of bin:	9 cR ₃₀₀₀

FIG. 2A

126.1		Next interval up	
◆	451.62 F	AFM067yc5	D12S79 Microsatellite anchor marker AFM067yc5
	454.24 P0.10	A009F32	KIAA0331 KIAA0331 gene product
	455.39 P0.37	sts-N33343	ESTs
	455.39 P1.15	SGC38179	ESTs
	455.70 P0.06	stSG54526	ESTs
	455.81 P1.35	stSG1522	ESTs
	455.86 P2.06	sts-T56610	Homo sapiens mRNA for KIAA0875 protein, p..
	456.02 P2.38	sts-R33659	EST
	456.34 P0.23	sts-D29101	EST
	456.34 P0.04 *	SGC44506	ESTs
	456.86 P2.34	NIB1804	ESTs
	456.86 P>3.00	stSG44263	ESTs, Weakly similar to calcium-binding pr..
	456.86 "	stSG62560	Homo sapiens clone 24852 mRNA sequence
	456.96 P1.66 *	sts-AA001615	ESTs
	456.96 P0.04	sts-T94297	ESTs, Weakly similar to TBX2 gene [H.sapi..
	457.17 P1.31	stSG54365	ESTs
	457.17 P0.13	WI-21497	Homo sapiens mRNA for KIAA0875 protein, p..
	457.17 P0.30	WI-20357	Homo sapiens mRNA for KIAA0875 protein, p..
	457.17 P0.38	SGC31491	NOS1 nitric oxide synthase 1 (neuronal)
	457.17 P0.31	RK903_904	NOS1 nitric oxide synthase 1 (neuronal)
	457.17 P0.18	sts-AA007571	ESTs
	457.17 P1.35	stSG46223	ESTs
	457.17 "	stSG58387	ESTs
◆	457.27 P>3.00 *	Cda1ce05	Homo sapiens clone 23714 mRNA sequence
	457.27 P0.10 *	sts-W79390	NME2 non-metastatic cells 2, protein (NM23B) exp..
	457.48 P0.20	sts-Z40829	ESTs
	460.94 P0.00 *	A005Q47	ESTs
133.8	◆ 460.94 F	AFM351tb9	D12S366 Microsatellite anchor marker AFM351tb9
		Next interval down	

FIG. 2B



The interval shown is on the GB4 map
See also: equivalent interval on G3 map

About This Interval

Top of interval: D12S366 (133.8 cM)
 Bottom of interval: D12S340 (147.5 cM)
 Genetic size of bin: 14 cM
 Physical size of bin: 21 cR₃₀₀₀

Next interval up					
133.8	◆	460.94 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9
		462.85 P1.00 *	stSG8109		ESTs
		462.85 "	sts-X75252	PBP	prostatic binding protein
		462.95 P1.04	sts-AA011374		Homo sapiens KIAA0431 mRNA, partial cds

FIG. 2C

463.77 P0.19	WI-16745		Human clone 37, 5cM region surrounding hepa..
◆ 463.77 P0.20	SGC33949	KIAA0262	KIAA0262 gene product
463.98 P0.02	A008B04		ESTs
463.98 "	stSG50309		ESTs
463.98 "	stSG49970		Homo sapiens mRNA for KIAA0875 protein, p..
463.98 P0.04	stSG27318		Human clone 23932 mRNA sequence
463.98 P0.08	R06295		EST
463.98 P1.33	sts-W56792		ESTs
464.08 P2.32	A007E48		ESTs
464.19 P1.28	A009U43		ESTs
464.29 P1.33	stSG3138		Homo sapiens mRNA for KIAA0949 protein, p..
464.39 P1.09	sts-F21636		Human DNA sequence from BAC 15E1 on chrom..
464.39 P1.13	stSG15685	KIAA0262	KIAA0262 gene product
464.39 "	RP_P0_1	RPLP0	Ribosomal protein large, P0
464.39 P1.09	stSG29626		ESTs
464.39 P1.14	stSG31407		Human DNA sequence from BAC 15E1 on chrom..
464.39 "	A001T32	PXN	paxillin
464.39 "	A001W18		H.sapiens mRNA for AMP-activated protein ..
464.39 "	WIAF-40		Human mRNA for KIAA0219 gene, partial cds
464.39 "	sts-T95105		ESTs
464.39 "	Cda0id01		ESTs
464.39 P1.13	stSG31431		ESTs, Moderately similar to (define not a..
◆ 464.39 " *	WI-13177		Homo sapiens clone 23714 mRNA sequence
464.39 "	IB1092		Homo sapiens clone 23714 mRNA sequence
464.39 "	T79466		ESTs
464.39 P1.18	stSG48379		ESTs
464.45 P1.05	KIAA0219		Human mRNA for KIAA0219 gene, partial cds
464.45 "	stSG40392		ESTs
464.45 "	stSG31586		H.sapiens mRNA for AMP-activated protein ..
◆ 464.49 P0.21	A006F12	KIAA0152	KIAA0152 gene product
464.49 P0.25	sts-AA002185	PXN	paxillin
464.49 P0.10	stSG48442		ESTs
464.49 "	sts-T16456		ESTs
464.49 "	stSG62260		ESTs

FIG. 2D

	464.49	"	NIB1331		ESTs
	464.49	"	WI-15518		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49	"	WIAF-1058		ESTs, Moderately similar to unknown [H.sap..
	464.49	"	SGC34758		ESTs
	464.49	"	WI-19738		Homo sapiens mRNA for KIAA0787 protein, p..
	464.49	"	IB383		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49	"	SGC32343		ESTs
	464.79	P0.96	SGC33521		ESTs
	464.79	P0.96	* X58965	NME2	non-metastatic cells 2, protein (NM23B) exp..
	465.20	P0.20	sts-H10302		ESTs
◆	465.38	P0.85	A007E11	KIAA0262	KIAA0262 gene product
	465.41	P0.81	A007I44	RPLP0	ribosomal protein, large, P0
	465.41	"	stSG22726		EST
	465.41	"	WI-17776		ESTs
	465.41	"	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41	"	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41	P0.77	stSG4775	SFRS9	splicing factor, arginine/serine-rich 9
	465.41	"	A002J47		ESTs, Weakly similar to heat shock protein..
	465.41	P0.80	stSG46660		EST
	465.51	P0.75	stSG41086	PXN	paxillin
	465.51	P0.83	stSG52121		ESTs
	465.91	P0.01	WI-16071		ESTs
	465.91	P0.00	WI-13962		H.sapiens mRNA for AMP-activated protein ..
	466.62	P0.00	sts-AA011220	SFRS9	splicing factor, arginine/serine-rich 9
	466.71	P0.00	stSG4712		ESTs, Weakly similar to homology with o251..
	466.91	P0.01	WI-15135		Homo sapiens mRNA for KIAA0787 protein, p..
	466.91	P0.01	D12S2088	TCF1	transcription factor 1, hepatic; LF-B1, hep..
	467.01	P0.01	stSG52567		ESTs
135.1	467.11	F	AFM123xh2	D12S86	Microsatellite marker AFM123xh2
135.1	467.11	P0.01	AFM299zd5	D12S349	Microsatellite marker AFM299zd5
	467.11	P0.01	AFM123xh2		Unknown
137.5	◆ 467.21	P0.02	AFM220zf4	D12S321	Microsatellite marker AFM220zf4
	467.21	P0.02	sts-W73277	SFRS9	splicing factor, arginine/serine-rich 9
	467.21	P0.02	stSG8721		EST

FIG. 2E

467.21 "	stSG44224		ESTs
467.21 "	stSG49978		H.sapiens mRNA for AMP-activated protein ..
◆ 467.21 "	stSG31862		Homo sapiens HSPC004 mRNA, complete cds
467.21 "	stSG47820		ESTs
467.21 "	Bdac4h06	KIAA0262	KIAA0262 gene product
467.21 "	stSG15021		ESTs
467.21 "	A002B13	SFRS9	splicing factor, arginine/serine-rich 9
◆ 467.21 "	H50549	KIAA0262	KIAA0262 gene product
467.21 P0.03	SGC35167		EST
467.21 P0.03	WI-19637		H.sapiens mRNA for AMP-activated protein ..
467.21 P0.02	WIAF-607		Unknown
467.31 P0.02	WI-16997	RPLP0	ribosomal protein, large, P0
468.93 P0.85	SGC31344		EST
469.13 P0.90	A007C39	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 ..
469.13 P0.14	stSG35104		ESTs
469.13 "	A006Q41		Unknown
469.23 P0.18	sts-Y07684	P2RX4	purinergic receptor P2X, ligand-gated ion c..
469.33 P0.93	stSG8506		ESTs, Moderately similar to unknown [H.sapi..
469.33 "	R01708		EST
469.33 "	stSG54819	HCALB_BR	calbrain
469.33 "	A001Z45		ESTs, Highly similar to (define not avail..
469.33 "	stSG35318		ESTs, Weakly similar to fos39554 1 [H.sapi..
469.33 "	stSG63173		EST
469.33 "	stSG31374	OASL	2'-5'oligoadenylate synthetase-like
469.42 P1.01	WI-16068		EST
469.44 P0.23	stSG1961		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62627		EST
469.44 "	stSG36007		Homo sapiens full length insert cDNA clone..
469.44 "	stSG39281	P2RX7	purinergic receptor P2X, ligand-gated ion c..
469.44 "	stSG2554		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62591		ESTs
◆ 469.54 P1.03	A006N38	KIAA0152	KIAA0152 gene product
469.62 P1.03	sts-N34573		ESTs
469.62 P1.03	sts-N58045		ESTs

FIG. 2F

469.62 P1.04		WI-13224		EST
469.83 P1.12		SGC34424		ESTs
469.93 P1.14		stSG3875	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.14 P1.17		stSG52516		ESTs, Weakly similar to (define not avail..
470.24 P1.32		D0S1735E		ESTs
470.24 P1.12		WI-6178		ESTs
470.32 P1.25		sts-U29895		Unknown
470.32 P1.24		WI-19611	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.43 P1.29		stSG52094		ESTs
470.63 P1.38		A004O17		ESTs
◆ 470.77 P1.32	**	SGC33451		ESTs, Weakly similar to rhoHP1 [H.sapiens..
◆ 470.84 P1.35	**	sts-X64838	RSN	restin (Reed-Steinberg cell-expressed inter..
470.84 P1.52		WI-13062		Homo sapiens mRNA, expressed in fibroblast..
471.27 P1.60		sts-R99269		EST
471.37 P1.70		stSG1991		ESTs
471.37 "		stSG15859		Homo sapiens full length insert cDNA YQ02..
471.58 P1.78		stSG29729		ESTs, Weakly similar to (define not avail..
471.58 P1.37		WI-16979		ESTs
471.65 P1.39		WI-17693		EST
471.80 P1.29		WI-22060		ESTs
471.90 P>3.00		stSG8210		ESTs, Moderately similar to neuronal threa..
471.90 "		WI-17956		EST
471.90 "		WI-20969		Homo sapiens mRNA for KIAA0867 protein, c..
471.90 "		stSG47029		ESTs
471.90 "		stSG47647		EST
471.90 "		sts-W45376		Homo sapiens mRNA for KIAA0867 protein, c..
◆ 471.90 "	**	WI-6021	RSN	restin (Reed-Steinberg cell-expressed inter..
471.90 "		NIB962		ESTs
471.90 "		A009E34		ESTs, Moderately similar to neuronal threa..
471.90 "		sts-T17477		ESTs
472.08 P1.49		sts-X89984		H.sapiens mRNA for BCL7A protein
472.12 P>3.00		SGC34693		EST
472.12 P>3.00		A009O01		ESTs, Weakly similar to neuronal thread pr..
472.29 P>3.00		stSG47084		ESTs

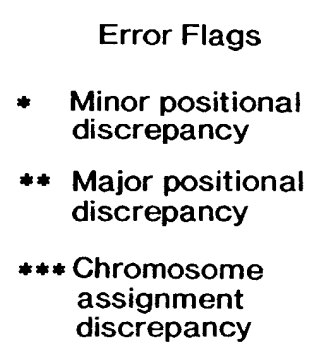
FIG. 2G

472.40 P>3.00	stSG58209	EEF1D	eukaryotic translation elongation factor 1 d..
472.40 P>3.00	AA213821	EEF1D	eukaryotic translation elongation factor 1 d..
472.61 P>3.00	A002R44		Unknown
472.61 P>3.00	SGC35850	EEF1D	eukaryotic translation elongation factor 1 d..
472.72 P0.01	sts-H98108		ESTs
472.97 P>3.00	WI-6239		ESTs
473.04 P>3.00	sts-H75490		ESTs
◆ 473.58 P>3.00 **	WI-14983	RSN	restin (Reed-Steinberg cell-expressed inter..
474.01 P>3.00	stSG8610		ESTs
474.01 P>3.00	stSG47080		ESTs
474.38 P2.18	stSG8686		ESTs, Weakly similar to similar to pre-mRN..
474.38 P2.25	stSG26358		ESTs, Weakly similar to similar to pre-mRN..
474.38 "	stSG29931		ESTs
474.38 "	WI-17926		ESTs
474.38 "	WI-12790		ESTs, Weakly similar to MULTIDRUG RESI..
474.38 "	1834		EST
474.38 P2.26	sts-X98258	MPP-9	M phase phosphoprotein 9
474.38 P2.39	stSG40753		ESTs
474.64 P>3.00	A004D47		ESTs, Highly similar to There are three pu..
474.64 P>3.00	sts-N23129	MPP-9	M phase phosphoprotein 9
474.75 P2.41	sts-AA040696		ESTs
474.81 P2.37	sts-AA022496		ESTs
474.81 P2.28	stSG46930	MPP-9	M phase phosphoprotein 9
474.97 P>3.00	WI-20552	DRP	density-regulated protein
475.02 P>3.00	SGC30324		ESTs
475.07 P>3.00	D10923	HM74	putative chemokine receptor; GTP-binding pr..
475.07 P>3.00	stSG2418	DOC1	Deleted in oral cancer-1
475.07 "	stSG21321		ESTs
475.07 "	stSG53515	MPP-9	M phase phosphoprotein 9
475.07 P>3.00	SGC31687	DOC1	Deleted in oral cancer-1
475.07 P>3.00	WIAF-214	HM74	putative chemokine receptor; GTP-binding pr..
475.13 P0.79	sts-W93806		ESTs
475.13 P2.13	stSG48145		ESTs
475.18 P2.34	A003B12		Homo sapiens full length insert cDNA clone..

FIG. 2H

	475.18 P>3.00	WI-22211		Homo sapiens full length insert cDNA clone..
	475.18 P2.08	stSG48093		ESTs
	475.18 "	A004P27		ESTs, Weakly similar to MULTIDRUG RESL..
	475.35 P2.10	stSG9904		ESTs
	475.40 P0.45	sts-AA024696		ESTs
	475.51 P>3.00	stSG53793		ESTs
	476.10 P>3.00	Bda98d05		Homo sapiens full length insert cDNA clone..
	476.21 P>3.00	sts-H24468		ESTs
	476.21 P>3.00	sts-N94741		ESTs
	476.64 P0.28	stSG22488		ESTs
	476.85 P0.36	stSG44909		ESTs
	477.06 P0.i0	stSG54797		ESTs
	477.27 P1.33	stSG48099		ESTs
	477.37 P0.09 *	sts-AA028894		Homo sapiens silencing mediator of retinoic..
	477.80 P1.44	stSG52727		EST
	477.80 "	U44799		Human U1-snRNP binding protein homolog mR..
	477.80 "	WI-15963		ESTs
	477.80 "	stSG53886		ESTs, Weakly similar to neuronal thread pr..
	478.74 P0.01	WIAF-364		ESTs
	479.01 P0.21	WI-21080		ESTs
	479.13 P0.19	A009B29		ESTs
	479.33 P0.22	A006F32	EIF2B1	eukaryotic translation initiation factor 2B..
	479.33 P0.19	WIAF-449	EIF2B1	eukaryotic translation initiation factor 2B..
	479.33 P0.19 *	WI-15890		H.sapiens mRNA for transmembrane protein r..
	479.55 P0.20 *	stSG349		H.sapiens mRNA for transmembrane protein r..
	479.55 " *	A004O46	BDKRB2	bradykinin receptor B2
	479.55 "	stSG42540		ESTs
	479.55 "	sts-N26791		ESTs
	479.55 "	stSG53943		ESTs
	479.55 "	stSG49468		EST
145.7	479.74 P0.16	AFM294ze9	D12S342	Microsatellite marker AFM294ze9
	481.46 P0.00	sts-AA007694		EST
147.5	481.56 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1
	Next interval down			

FIG. 2I

$$x = \begin{pmatrix} x_1 \\ x_2 \\ x_3 \end{pmatrix}, \quad A = \begin{pmatrix} 1 & -1 & 0 \\ 0 & 1 & 1 \\ 0 & 0 & 1 \end{pmatrix}, \quad b = \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix}$$


See also: equivalent interval on G3 map

Top of interval:	D12S340 (147.5 cM)
Bottom of interval:	D12S97 (160.9 cM)
Genetic size of bin:	13 cM
Physical size of bin:	13 cR ₃₀₀₀

Position (cM)	Marker	Marker Type	Marker Name
147.5	481.56 F	Microsatellite anchor marker	AFM294xg1
481.66 P0.00	SGC31838	ESTs	D12S340
483.18 P0.70	stSG48255	ESTs	
483.58 P0.69	stSG47315	ESTs	

FIG. 2J

483.87	P0.83	stSG47707		ESTs
484.70	P0.93	stSG4060		ESTs
484.70	"	stSG62390	GTF2H3	general transcription factor IIH, polypepti..
484.70	"	stSG42994		ESTs
484.73	P0.74	stSG46906		ESTs
484.80	P0.91	A004X33		ESTs
484.91	P1.11	stSG3211		ESTs, Weakly similar to B-cell growth fact..
484.91	"	* sts-Z41302	BDKRB2	bradykinin receptor B2
484.91	"	* sts-Z41302	BDKRB2	bradykinin receptor B2
484.91	"	sts-T58259		ESTs, Weakly similar to B-cell growth fact..
484.91	"	stSG52737		ESTs
484.91	"	Bda03b10	UBC	ubiquitin C
484.91	"	stSG1936	CD36L1	CD36 antigen (collagen type I receptor, thr..
484.91	"	sts-AA017225		ESTs
484.91	P1.15	WI-12212		ESTs
485.12	P1.18	A004F14		ESTs
485.12	P1.18	SGC31333		ESTs
485.23	P1.21	* WI-12482	BDKRB2	bradykinin receptor B2
485.23	P1.07	sts-AA017698		ESTs
485.33	P1.22	WI-12422		ESTs
485.51	P1.18	stSG42398		EST
485.64	P1.04	sts-AA009669		ESTs
486.07	P2.50	stSG21539		EST
486.13	P1.44	WI-12439		EST
486.34	P1.26	sts-W31616	UBC	ubiquitin C
486.38	P>3.00	stSG54715		ESTs
486.76	P1.64	* WI-6921		H.sapiens mRNA for transmembrane protein r..
487.08	P>3.00	WI-13120		Human mRNA for KIAA0318 gene, partial cds
487.23	P>3.00	stSG54353		ESTs
487.23	P>3.00	stSG22703		EST
487.28	P>3.00	stSG62698		ESTs
487.28	P>3.00	* sts-D60472		Homo sapiens silencing mediator of retinoic..
487.28	P>3.00	stSG36097		ESTs
487.33	P1.36	sts-U37146		Homo sapiens silencing mediator of retinoic..

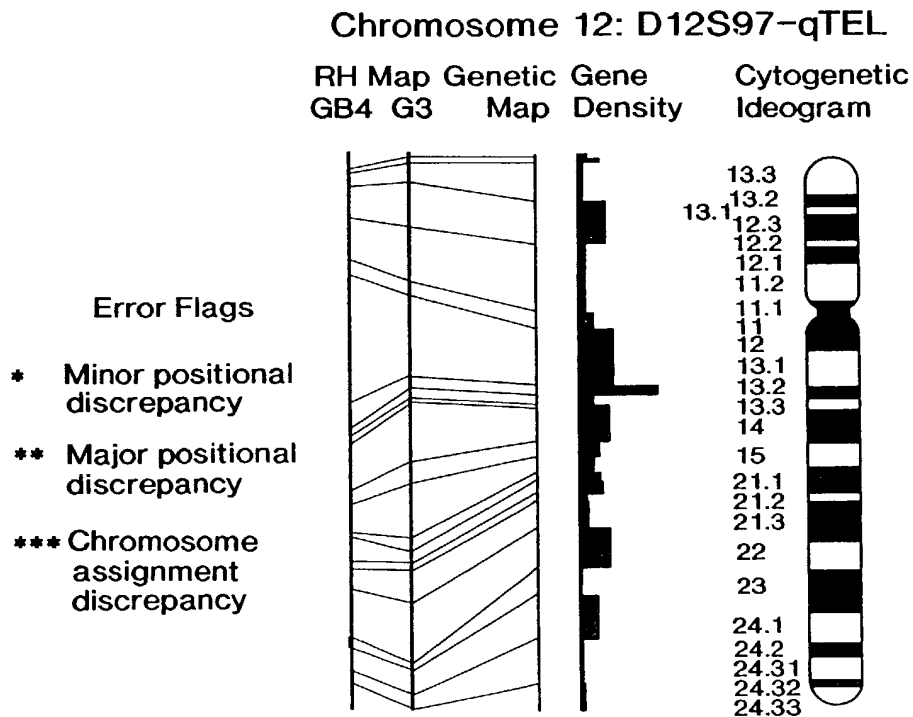
FIG. 2K

	487.50 P>3.00	stSG9807	ESTs
	487.50 P>3.00	stSG15434	ESTs
	487.60 P>3.00	stSG53251	ESTs
	487.60 P>3.00	stSG30525	SRRP129 SC35-interacting protein 1
	487.60 P>3.00	stSG46424	ESTs
	487.70 P>3.00	A007A34	ESTs
154.4	487.75 P2.00	AFMa197zd9	D12S1609 Microsatellite marker AFMa197zd9
	487.75 P2.02	A006D44	ESTs
	487.80 P>3.00	SGC30248	ESTs, Weakly similar to peptide/histidine ..
	488.07 P1.68	stSG6320	Homo sapiens clone 24617 mRNA sequence
	488.07 P1.66	stSG6305	Homo sapiens clone 24790 mRNA sequence
	488.07 P0.02	sts-N20163	Homo sapiens full length insert cDNA clone..
	488.12 P>3.00	stSG60065	ESTs
	488.12 P>3.00	stSG47723	ESTs
	488.44 P1.59	stSG3292	Homo sapiens clone 24790 mRNA sequence
	488.44 P0.03	WIAF-856	EST, Weakly similar to reverse transcripta..
	488.65 P1.54	WI-12272	Homo sapiens clone 24790 mRNA sequence
	488.65 P1.82	stSG52343	ESTs
	488.82 P1.80	stSG16387	CPN2 carboxypeptidase N, polypeptide 2, 83kD
	488.97 P1.80	SGC31722	ESTs
	489.07 P0.06	stSG54325	ESTs
	489.07 P>3.00	stSG63473	ESTs
160.9	◆ 489.07 P>3.00	AFMa123xe1	D12S367 Microsatellite marker AFMa123xe1
	489.14 P0.17	sts-T81113	ESTs
	489.29 P0.05	sts-AA025438	EST
	489.50 P1.37 ***	Cda1ad08	ESTs
	489.50 P0.05	WI-15018	ESTs
	489.50 P1.50	WI-18492	ESTs
	489.57 P1.48	WI-16177	Homo sapiens androgen receptor associated p..
	489.67 P1.44	stSG53307	ESTs
	489.71 P1.43	stSG53541	Homo sapiens hiwi mRNA, partial cds
	489.71 P1.43	stSG9546	Homo sapiens clone 24617 mRNA sequence
	489.89 P1.56	A006O16	ESTs
	490.10 P1.42	H64839	EST

FIG. 2L

stSG43910	SFRS8	splicing factor, arginine/serine-rich 8 (sup..
AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6

FIG. 2M



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval: D12S97 (160.9 cM)
 Bottom of interval: chr12_qTEL (169.1 cM)
 Genetic size of bin: 8 cM
 Physical size of bin: 172 cR3000

Next interval up				
160.9	◆	494.19 F	AFM210zd6	D12S97
		498.06 P0.02	stSG53600	
		499.71 P1.73	stSG3357	
165.7		499.71 "	AFM295ye9	D12S343
			Microsatellite anchor marker AFM210zd6	
			ESTs, Weakly similar to peptide/histidine ..	
			ESTs	
			Microsatellite marker AFM295ye9	

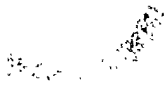
FIG. 2N

499.71 P1.72	stSG30906	ESTs
499.71 "	stSG43796	MMP17 matrix metalloproteinase 17 (membrane-insert..
499.71 P1.71	sts-X89576	MMP17 matrix metalloproteinase 17 (membrane-insert..
499.92 P>3.00	stSG43769	ESTs
500.50 P1.88	stSG26056	ESTs
500.50 P2.33	SGC30786	KIAA0331 KIAA0331 gene product
500.61 P>3.00	stSG1702	Homo sapiens CAGH32 mRNA, partial cds
500.61 "	sts-N59820	ESTs
500.61 "	stSG42115	KIAA0331 KIAA0331 gene product
500.61 "	IB2452	ULK1 unc-51 (C. elegans)-like kinase 1
500.61 "	stSG52521	ESTs
500.61 "	FB9F8	ESTs, Weakly similar to PUTATIVE ATP-D..
500.61 "	AA252357	ESTs
500.61 "	stSG4720	Homo sapiens pseudouridine synthase 1 (PUS..
500.61 "	sts-AA001424	KIAA0331 KIAA0331 gene product
500.61 P>3.00	stSG31443	ESTs
500.61 P>3.00	stSG49622	ULK1 unc-51 (C. elegans)-like kinase 1
500.61 P2.49	stSG50559	ESTs
501.04 P1.10	stSG54842	ESTs
501.04 P2.03	A008Y05	Unknown
501.89 P2.18	stSG39493	Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	A002A44	Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	sts-H94865	EST
501.99 P>3.00	R50113	ESTs
502.10 P1.75	stSG48386	ESTs
502.10 "	stSG50504	ESTs
502.63 P0.06	A006R19	ESTs
502.63 P1.06	WIAF-864	ESTs
502.94 P1.51	stSG54813	ESTs, Weakly similar to peroxisome membran..
503.04 P1.42	A004B47	ESTs, Highly similar to DNA polymerase ep..
503.25 P0.28	stSG27206	ESTs
503.25 "	stSG40199	Homo sapiens mRNA for KIAA0692 protein, p..
503.46 P0.23	stSG8935	ESTs
504.68 P0.69	stSG4731	Homo sapiens mRNA for KIAA0692 protein, p..

FIG. 20

169.1	504.68	"	A005Q05		ESTs
	504.68	"	stSG8142		ESTs, Highly similar to DNA polymerase ep..
	506.39	F	AFM310vd5	D12S357	Microsatellite marker AFM310vd5
	506.39	P0.02	A005X42		Homo sapiens mRNA for KIAA0692 protein, p..
	508.59	P0.78	Cda18g06		ESTs
	◆ 508.59	P0.78 **	Cda1jf08		Homo sapiens mRNA for GCP170, complete cd..
	508.59	P0.54	R39599		ESTs
	509.98	P0.10	stSG31494	ZNF140	zinc finger protein 140 (clone pHZ-39)
	509.98	P0.16	stSG40222		ESTs
	509.98	"	sts-R55615		ESTs, Weakly similar to zinc finger protei..
	509.98	"	sts-R02295		ESTs
	509.98	"	sts-R81342		ESTs
	511.20	F	TEL-12q82		Marker TEL-12q82
	512.81	P0.20	sts-H65839		ESTs, Weakly similar to transformation-rel..
	514.97	P0.36	stSG46141		ESTs, Weakly similar to zinc finger protei..
	514.97	P0.90	stSG52998		ESTs
	519.10	P1.77	A008W21	CYP51	cytochrome P450, 51 (lanosterol 14-alpha-de..
	519.54	P0.81	stSG52716		ESTs
	● TELOMERE				

FIG. 2P

[illegible]

See also: equivalent interval on GB4 map

Top of interval:	D12S79 (126.1 cM)
Bottom of interval:	D12S366 (133.8 cM)
Genetic size of bin:	8 cM
Physical size of bin:	63 cR ₁₀₀₀₀

FIG. 3A

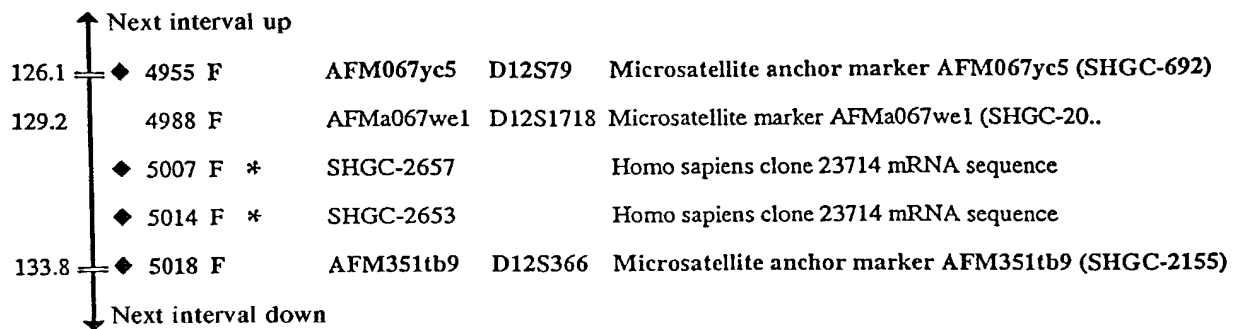
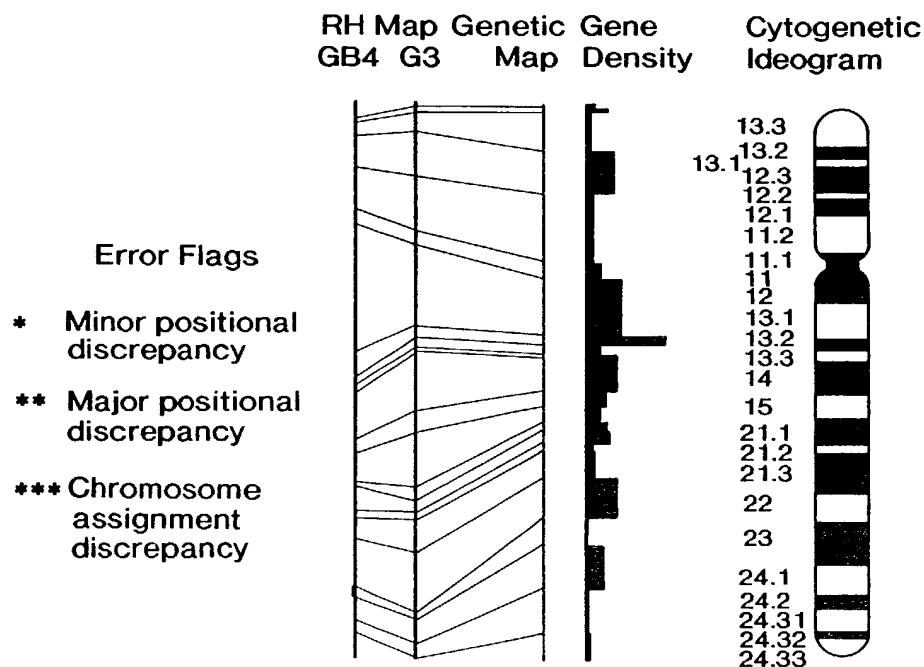


FIG. 3B

Chromosome 12: D12S366-D12S340



The interval shown is on the G3 map
See also: equivalent interval on GB4 map

About This Interval

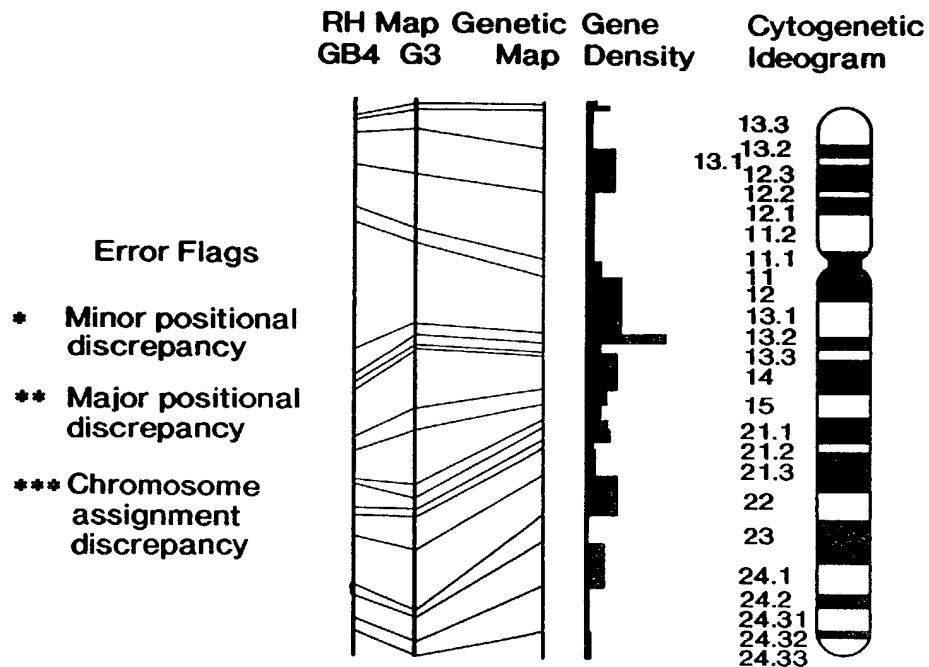
Top of interval: D12S366 (133.8 cM)
Bottom of interval: D12S340 (147.5 cM)
Genetic size of bin: 14 cM
Physical size of bin: 261 cR₁₀₀₀₀

FIG. 3C

133.8	↑ Next interval up	◆ 5018 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9 (SHGC-2155)
135.1		5047 F	AFMa225xe5	D12S1619	Microsatellite marker AFMa225xe5 (SHGC-20..
		◆ 5085 F	SHGC-33949	KIAA0262	KIAA0262 gene product
		◆ 5089 F	SHGC-10488	KIAA0152	KIAA0152 gene product
		◆ 5093 F	SHGC-10346		Homo sapiens HSPC004 mRNA, complete cds
		◆ 5098 F	SHGC-13898		Homo sapiens HSPC004 mRNA, complete cds
137.5		◆ 5163 F	AFM220zf4	D12S321	Microsatellite marker AFM220zf4 (SHGC-212..
		5199 F	SHGC-11702		ESTs
147.5	↓ Next interval down	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)

FIG. 3D

Chromosome 12: D12S340-D12S97



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S340 (147.5 cM)
 Bottom of interval: D12S97 (160.9 cM)
 Genetic size of bin: 13 cM
 Physical size of bin: 151 cR₁₀₀₀₀

FIG. 3E

					Next interval up
147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)	
148.3	5288 F	AFM234tb10	D12S324	Microsatellite marker AFM234tb10 (SHGC-21..	
154.4	5316 F	AFMb350zb5	D12S1679	Microsatellite marker AFMb350zb5 (SHGC-20..	
149.5	5358 F	AFM198wh2	D12S307	Microsatellite marker AFM198wh2 (SHGC-211..	
157.2	5393 F	AFMb301we5	D12S1659	Microsatellite marker AFMb301we5 (SHGC-20..	
160.9	◆ 5415 F	AFMa123xe1	D12S367	Microsatellite marker AFMa123xe1 (SHGC-21..	
160.9	◆ 5430 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6 (SHGC-372)	

FIG. 3F

$$= \frac{1}{\Gamma(\alpha)} \int_0^t (t-\tau)^{\alpha-1} d\tau = \frac{1}{\Gamma(\alpha)} \int_0^t (t-\tau)^{\alpha-1} \delta(\tau) d\tau$$

- * Minor positional discrepancy
- ** Major positional discrepancy
- *** Chromosome assignment discrepancy

About This Interval




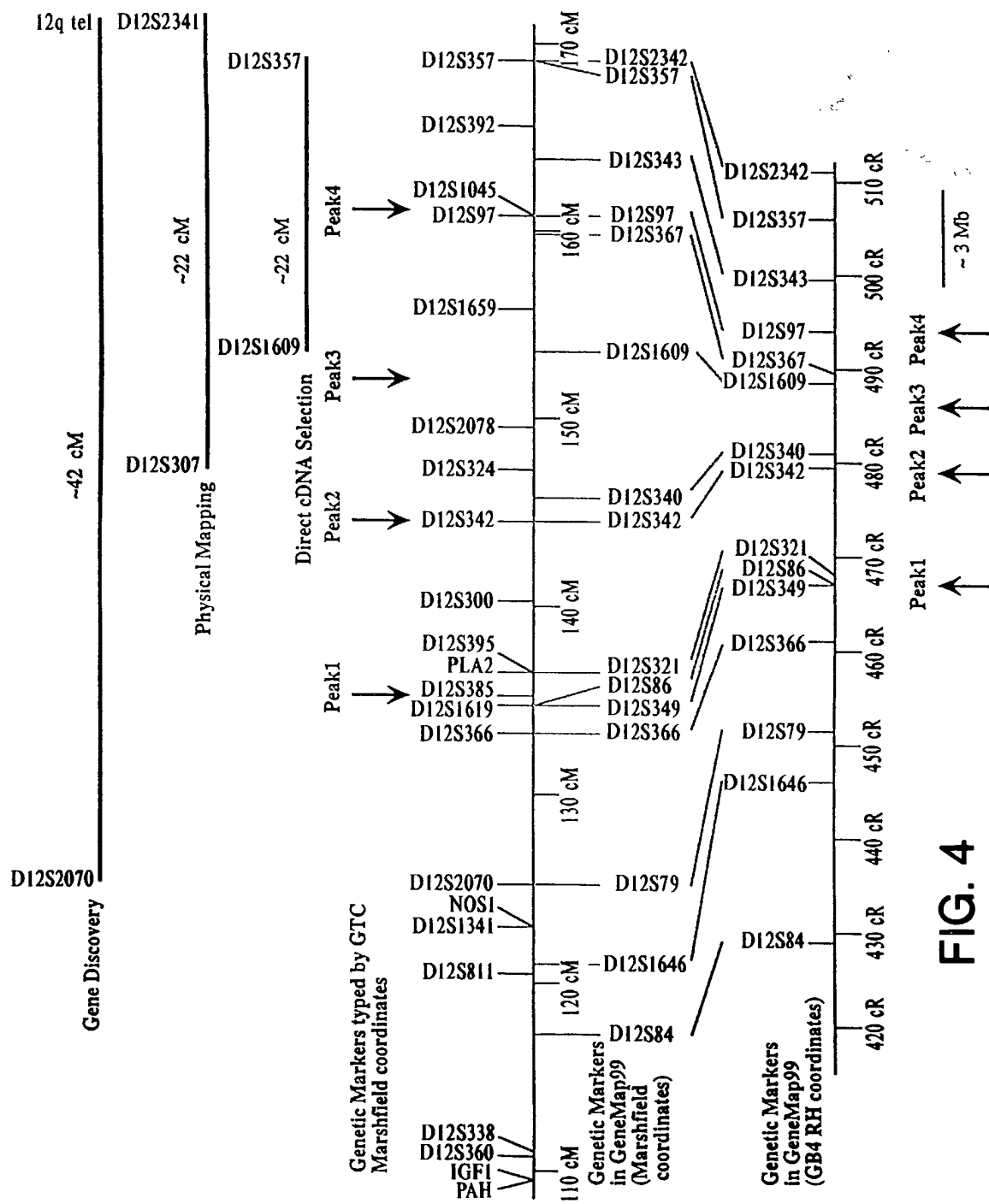
160.9  Next interval up
160.9  5430 F AFM210zd6 D12S97 Microsatellite anchor marker AFM210zd6 (SHGC-372)
 TELOMERE

FIG. 3G



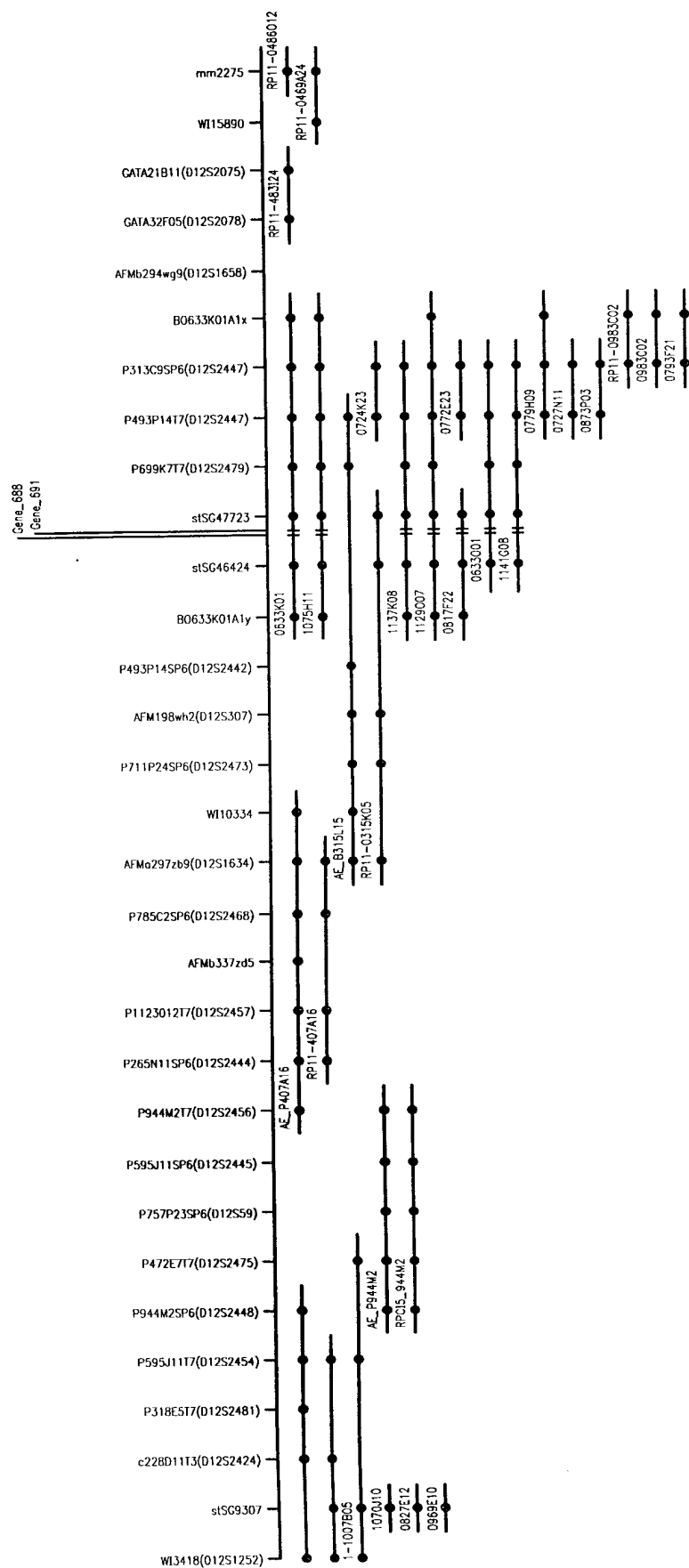


FIG. 5A

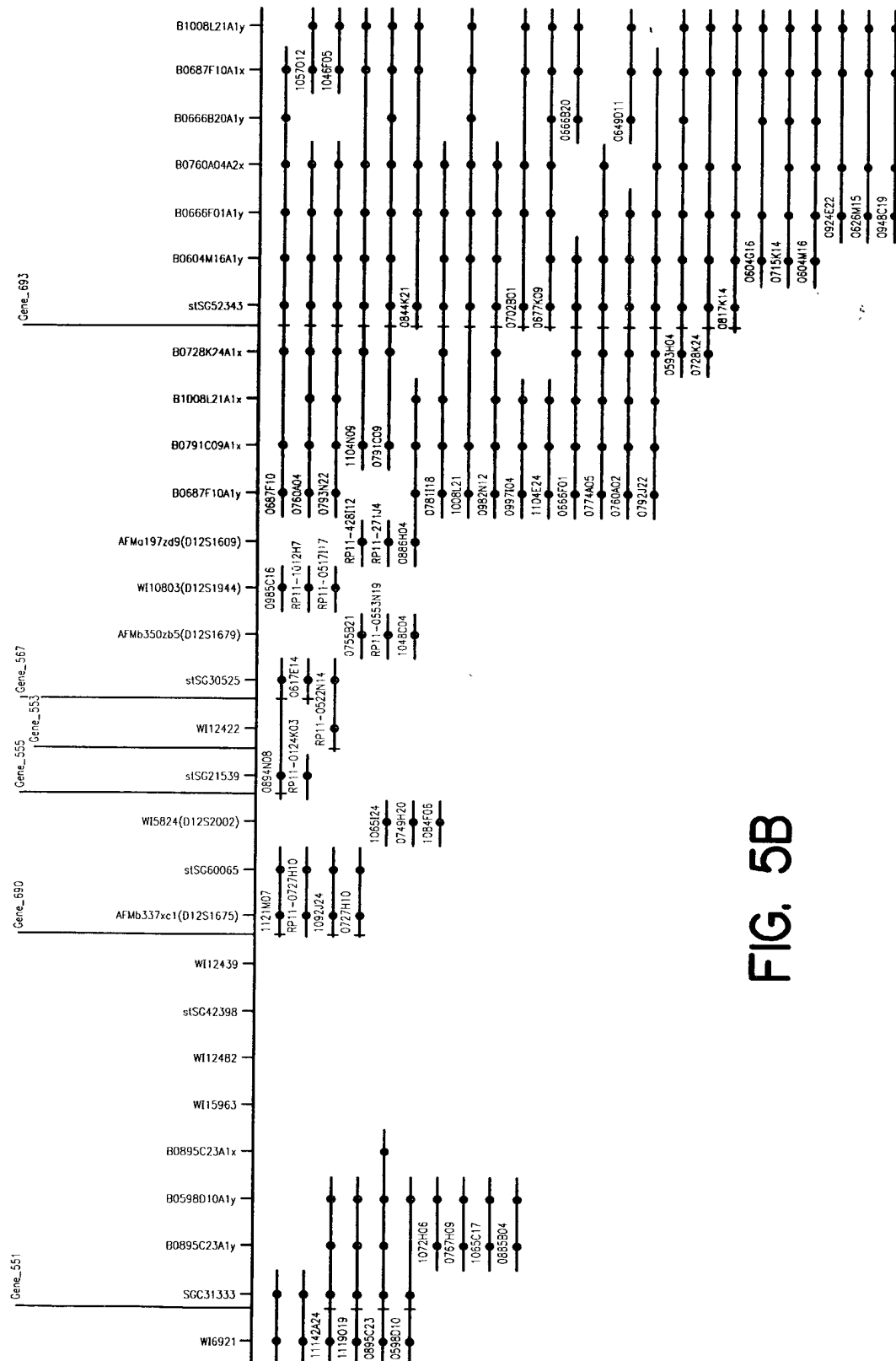


FIG. 5B

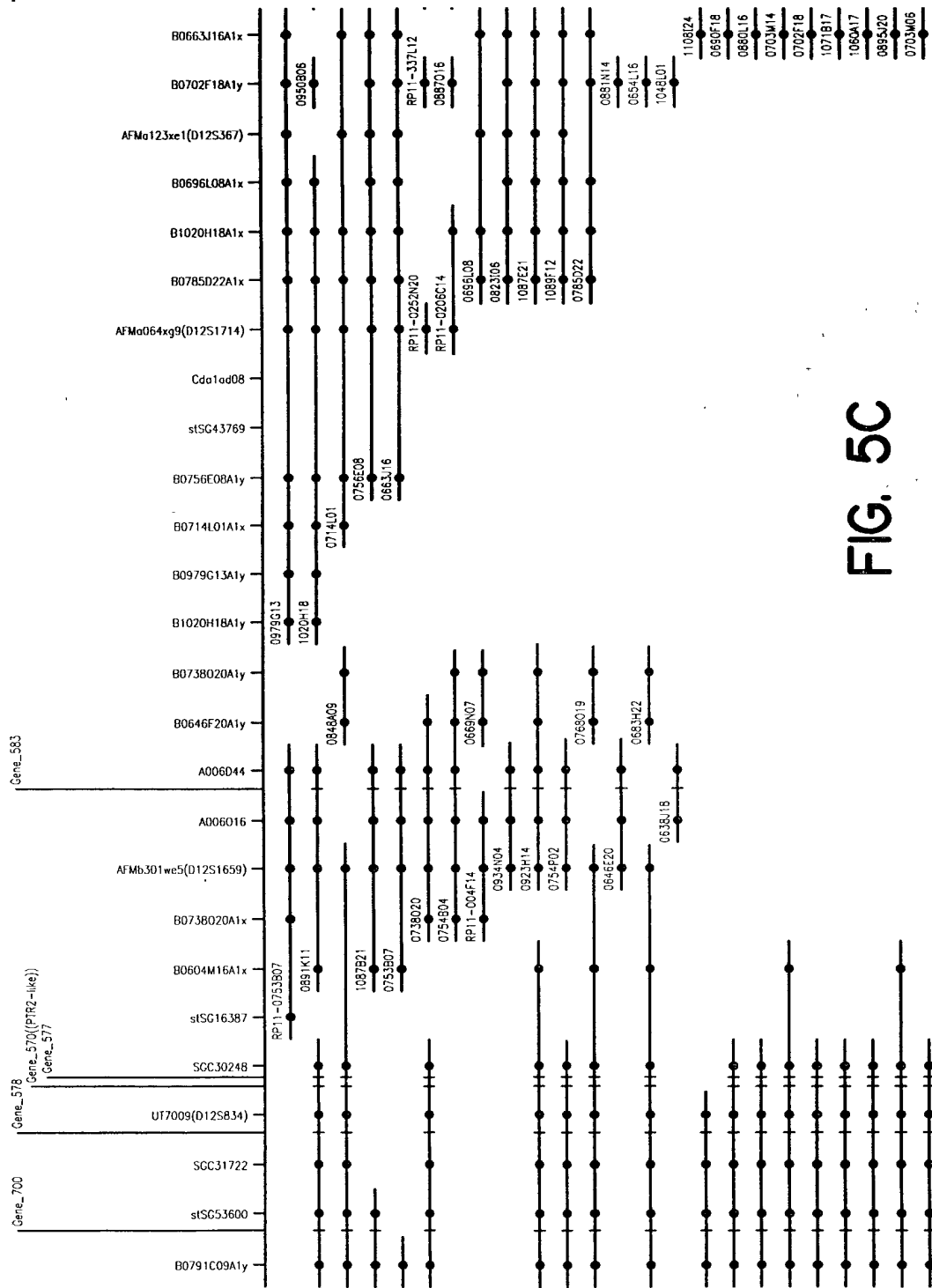
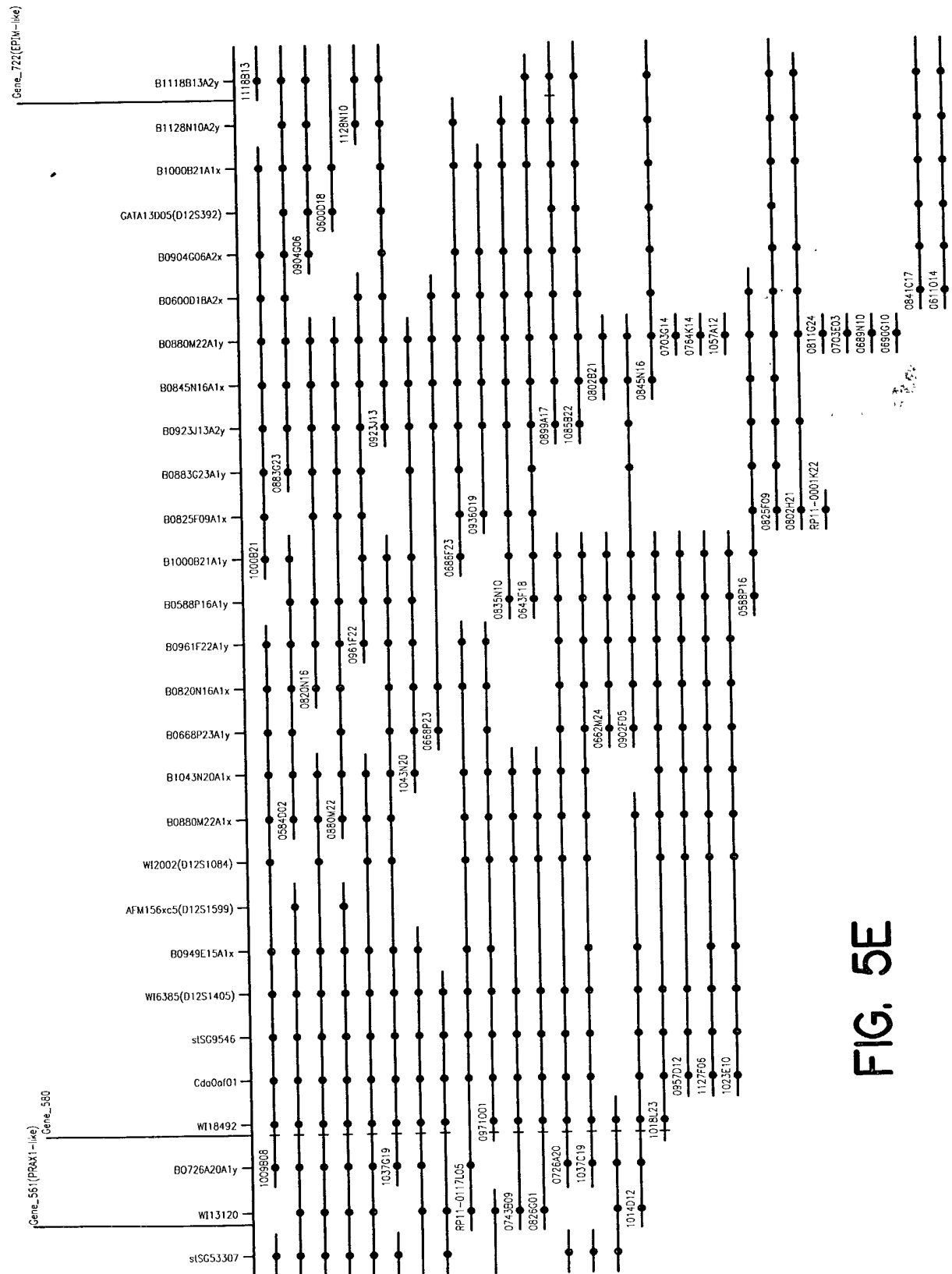
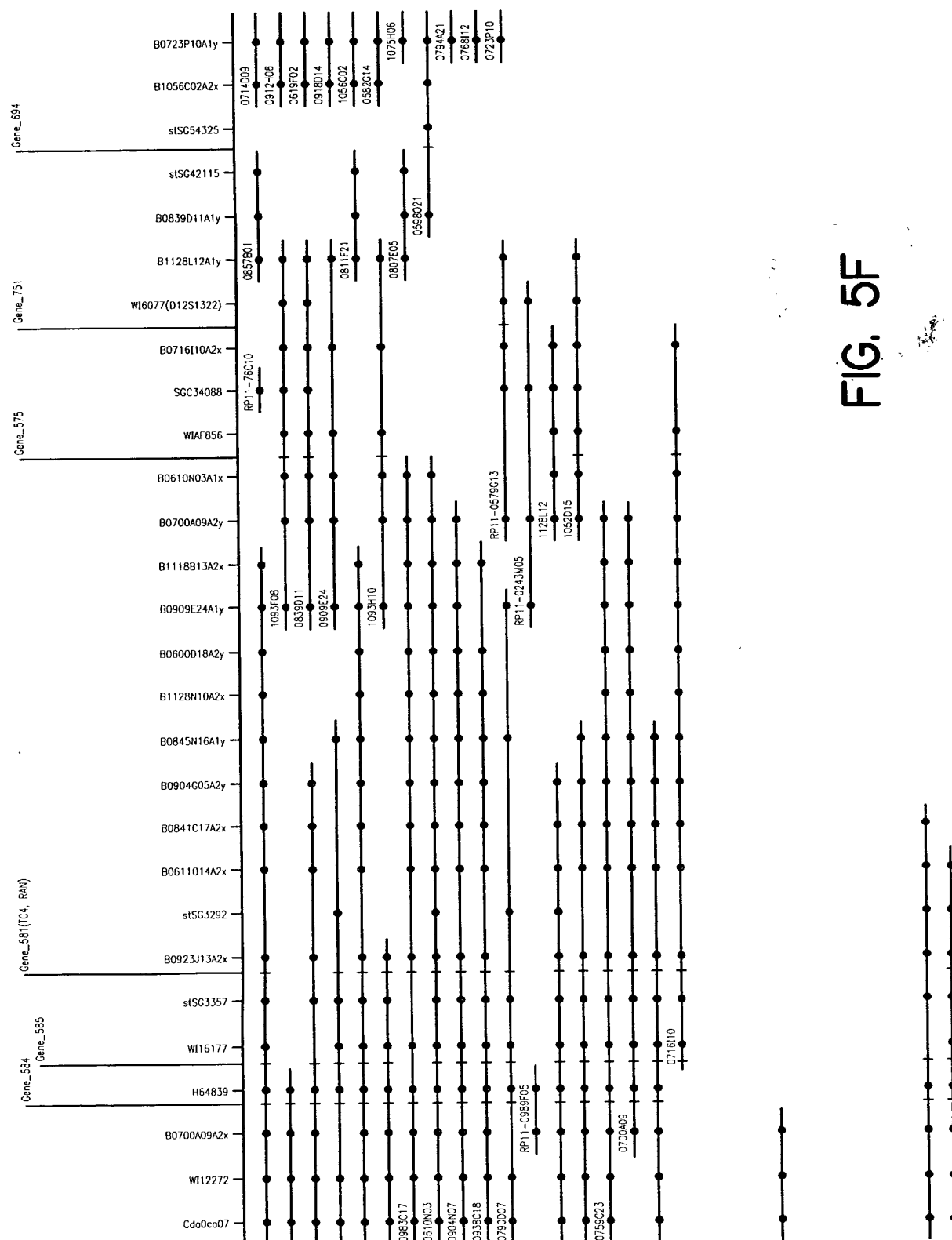


FIG. 5C







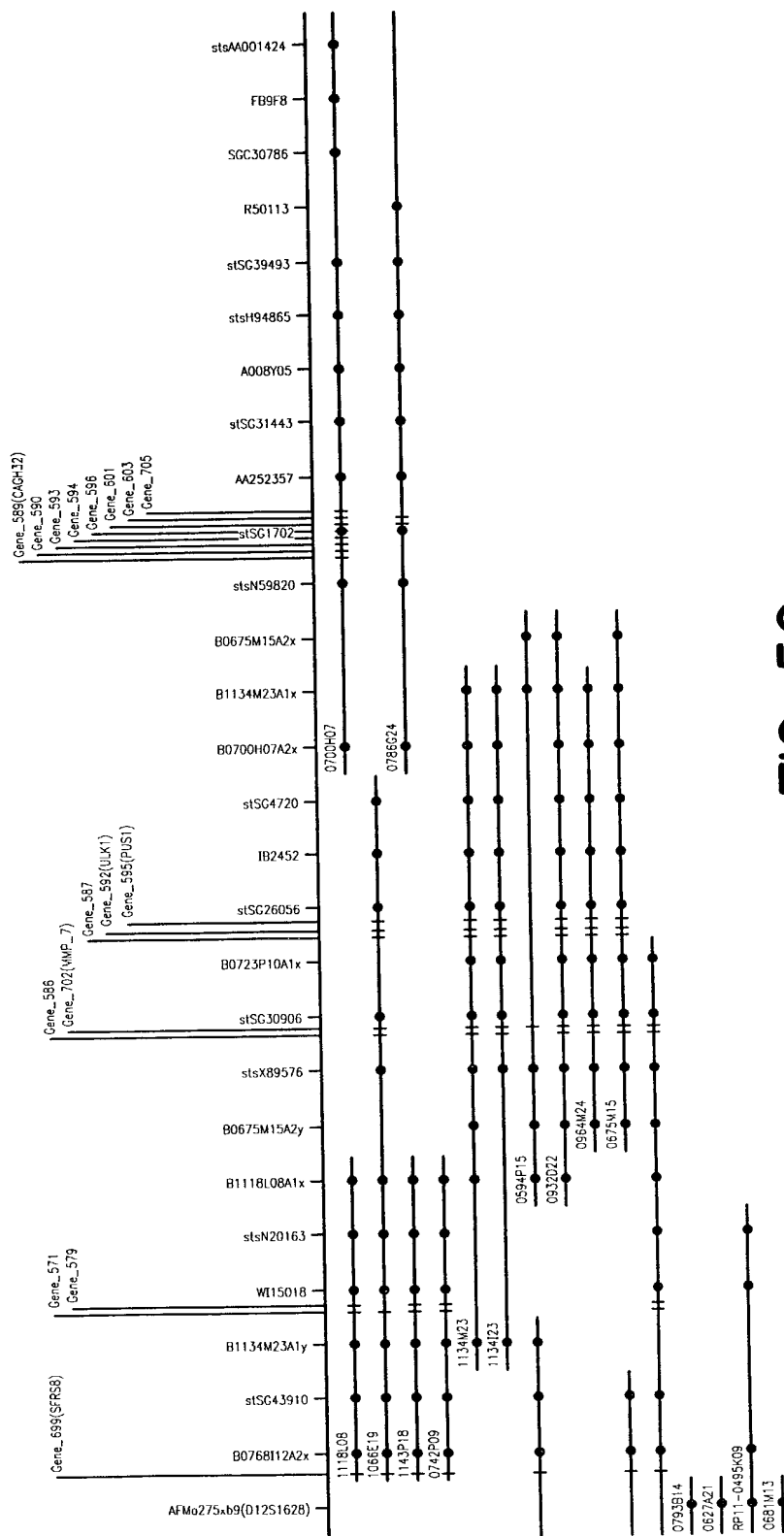
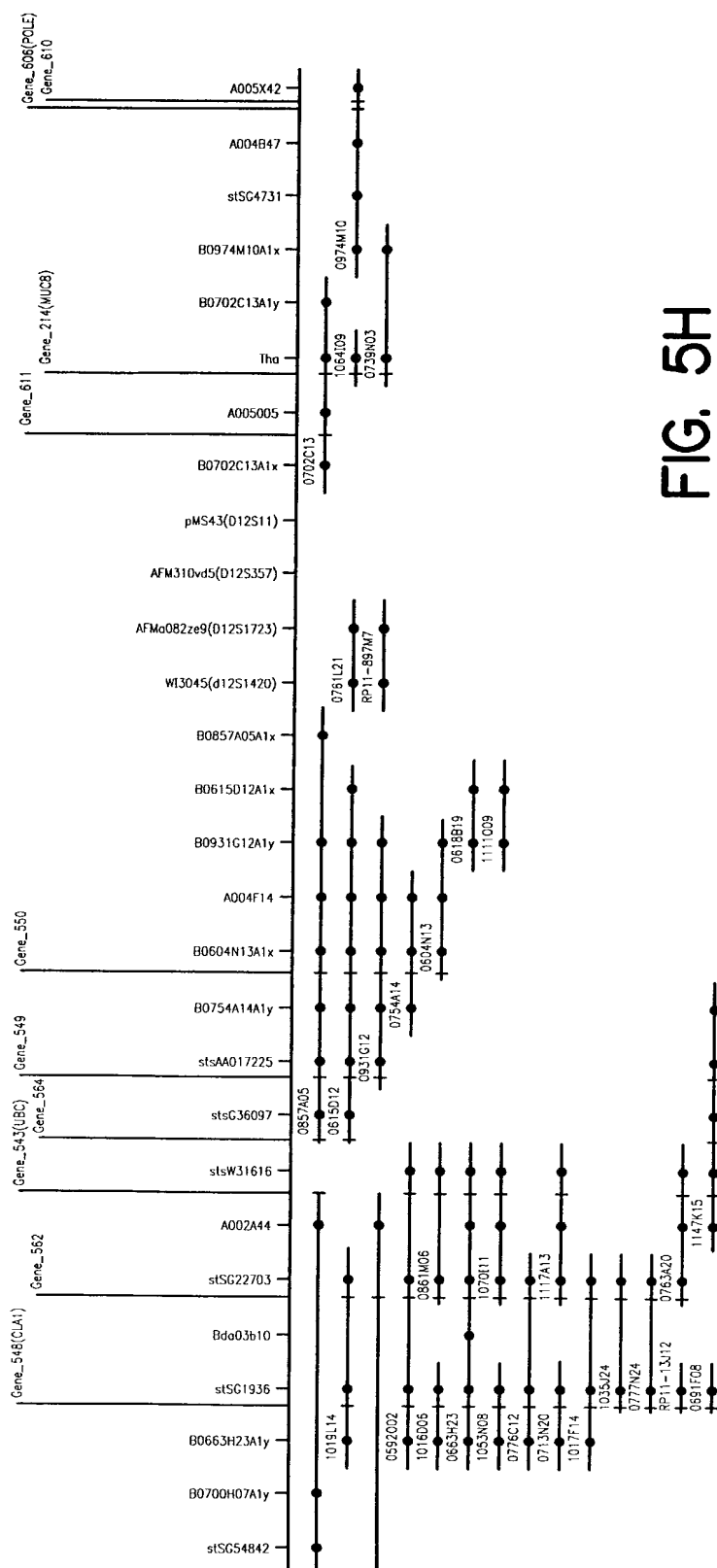


FIG. 5G



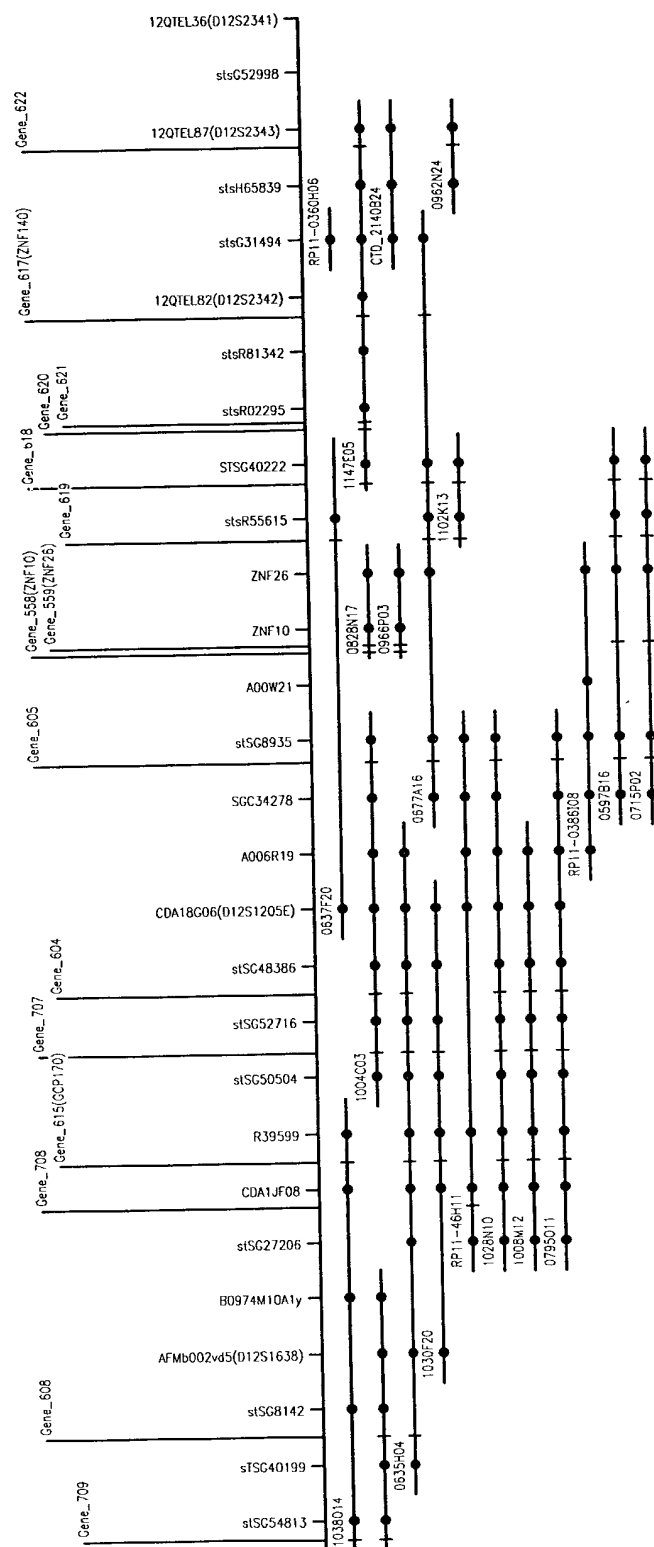
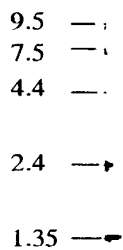


FIG. 51

Gene 214

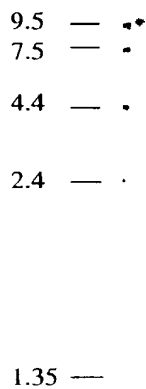
1 2 3



1. Lymphoblastoid cell line
2. Lung
3. Trachea

Gene 436

1 2 3 4 5 6 7 8 9 10 11 12



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6A

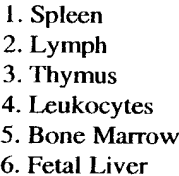
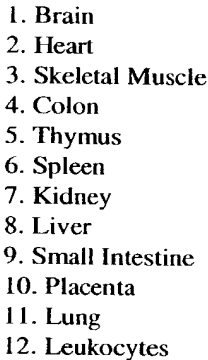
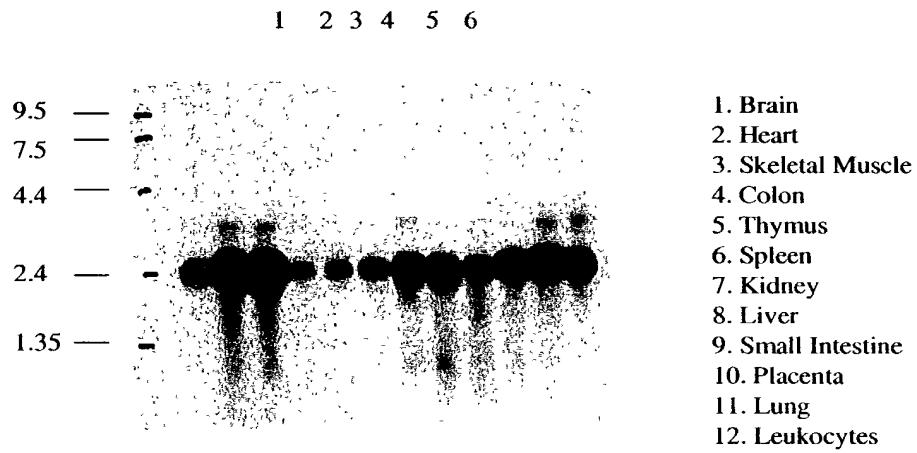
[illegible][illegible]

FIG. 6B

Gene 543



Gene 548

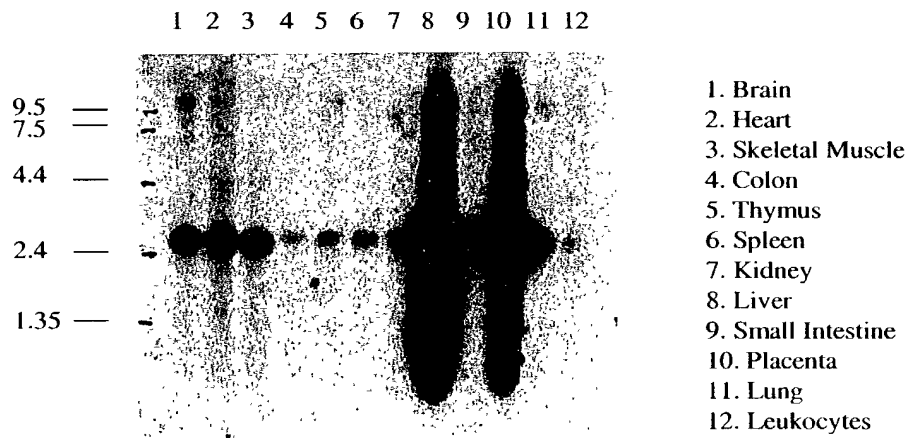
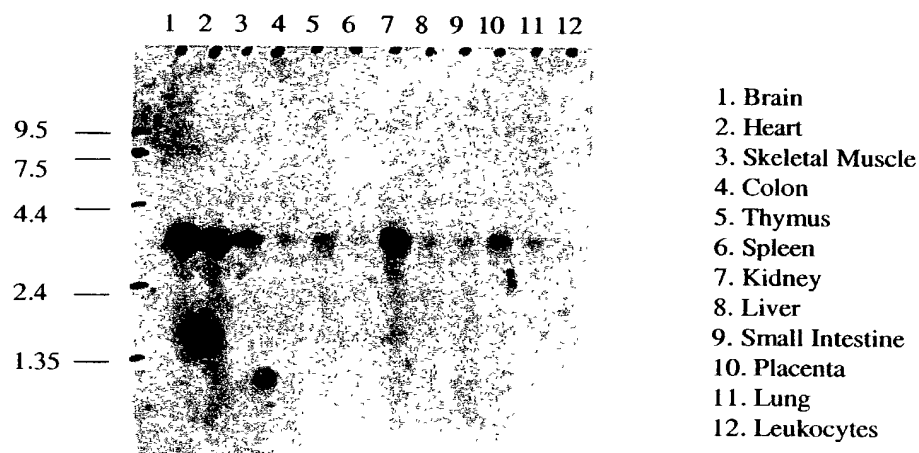


FIG. 6C

$$= \frac{1}{\beta} \left(\frac{\partial^2}{\partial t^2} + \frac{\partial^2}{\partial x^2} - \frac{\partial^2}{\partial y^2} - \frac{\partial^2}{\partial z^2} \right) \psi = \frac{1}{\beta} \nabla^2 \psi$$


Gene 561

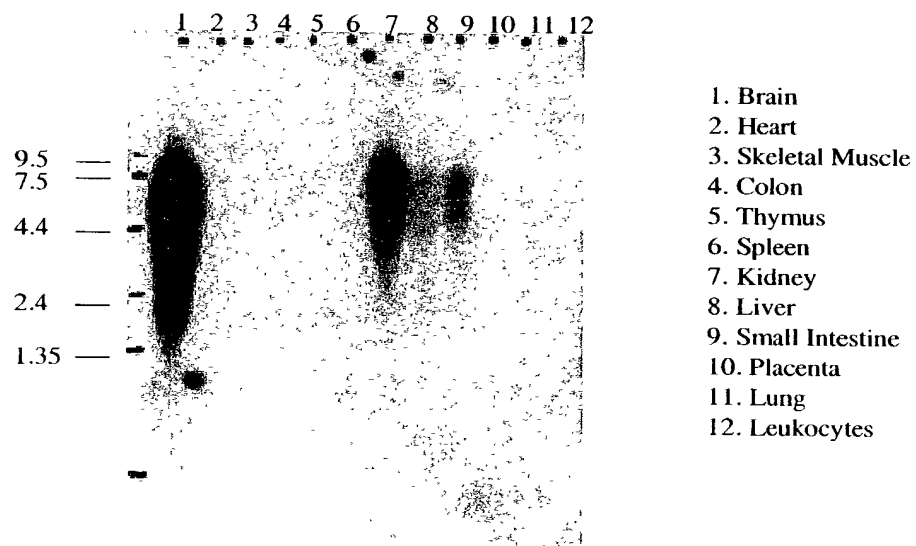
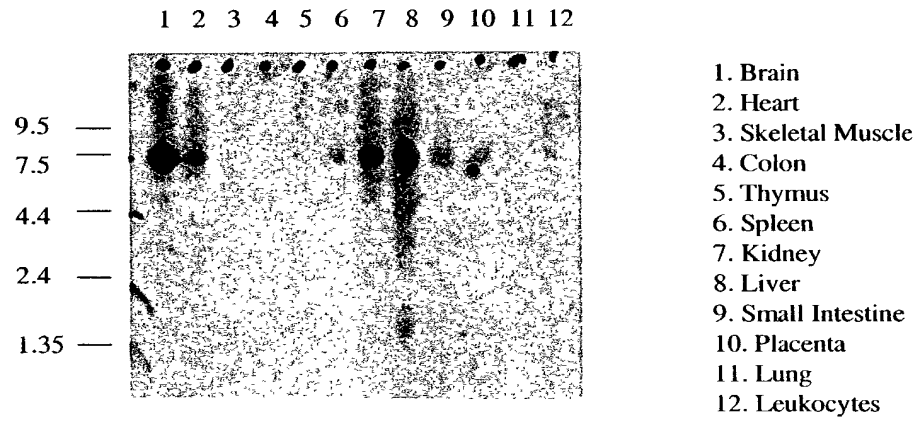


FIG. 6D

Gene 564



Gene 570

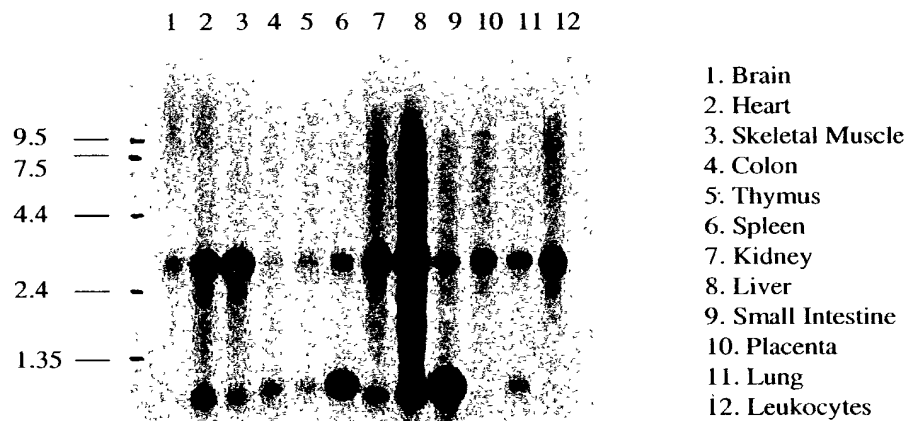
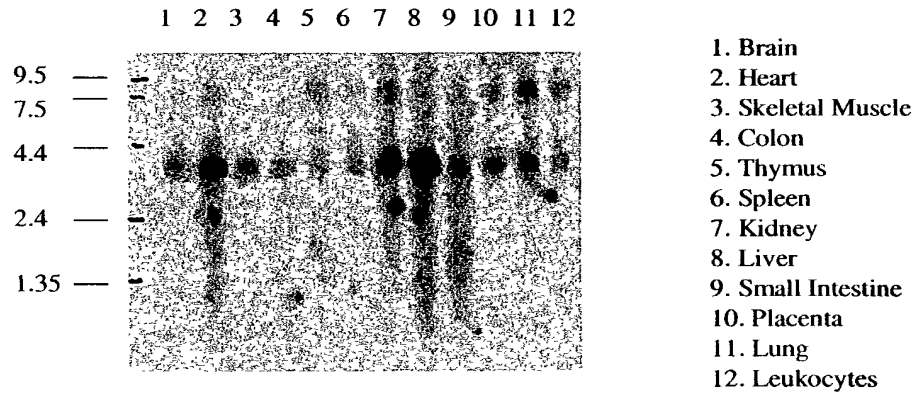


FIG. 6E

Gene 576

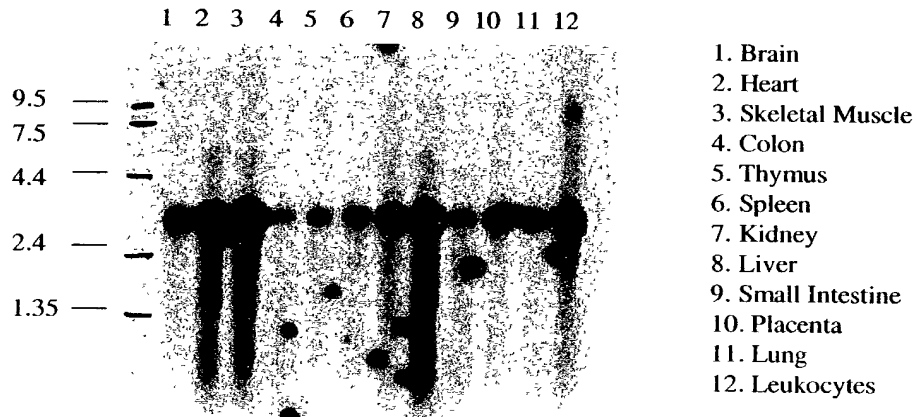


Gene 577



FIG. 6F

Gene 578



Gene 579

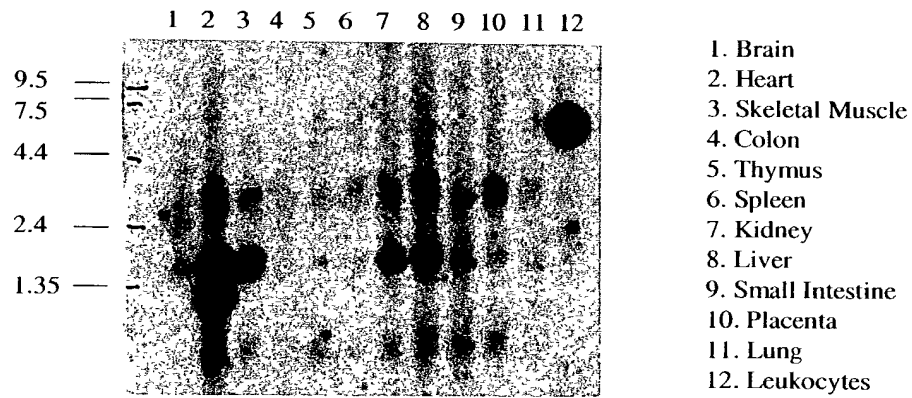
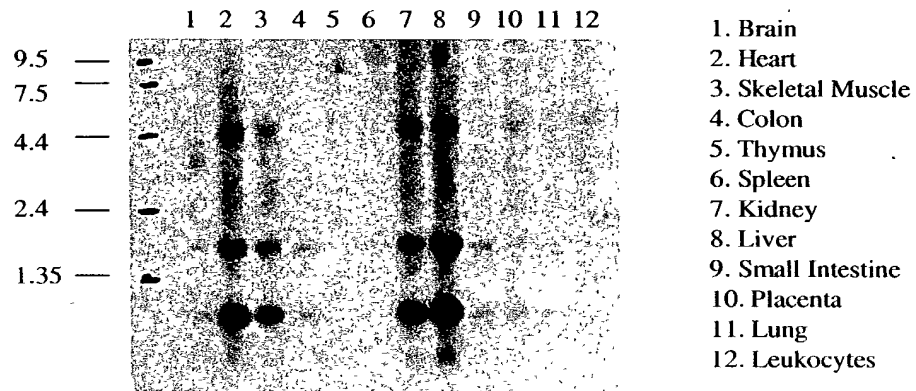


FIG. 6G

Gene 580



Gene 581

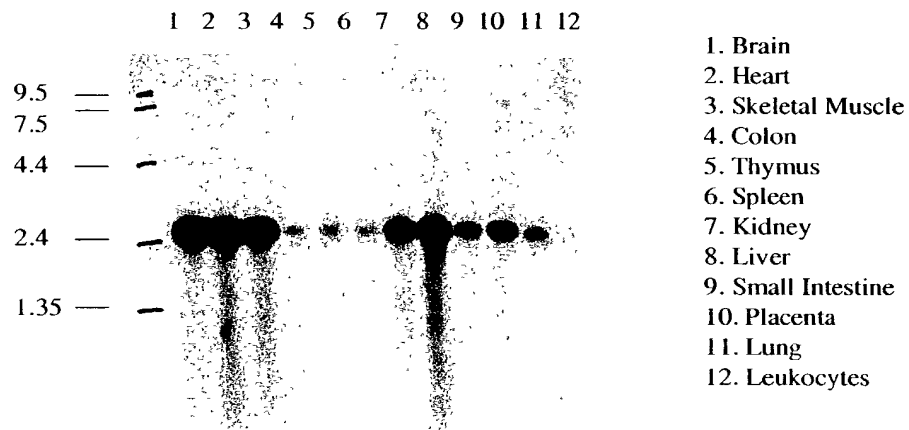
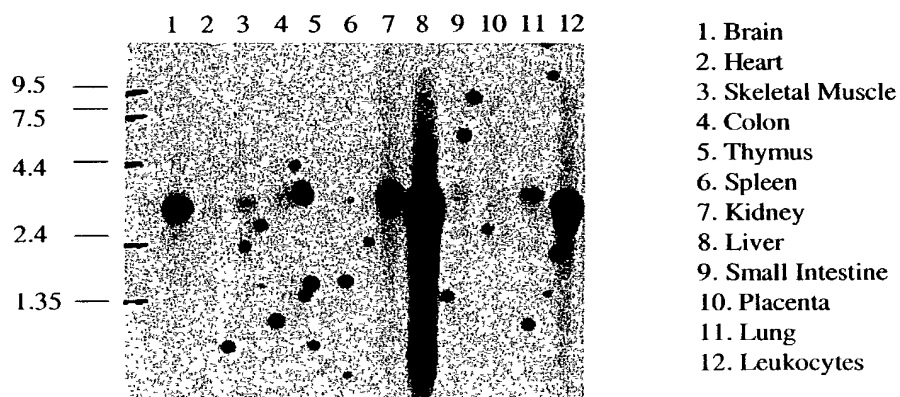


FIG. 6H

Gene 583



Gene 589

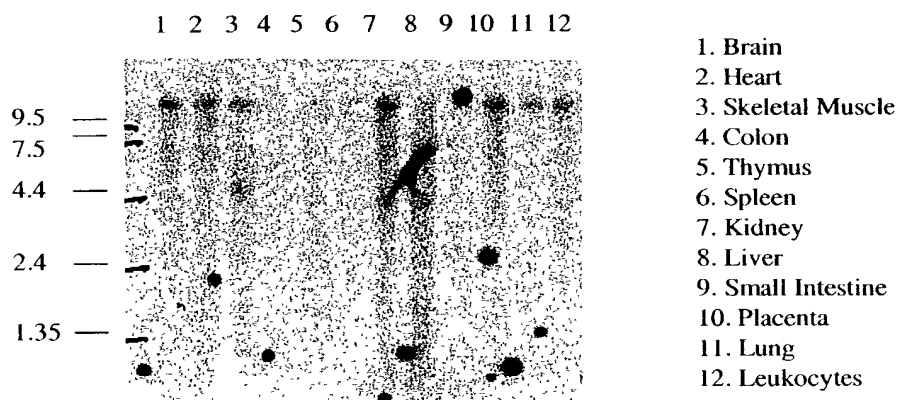
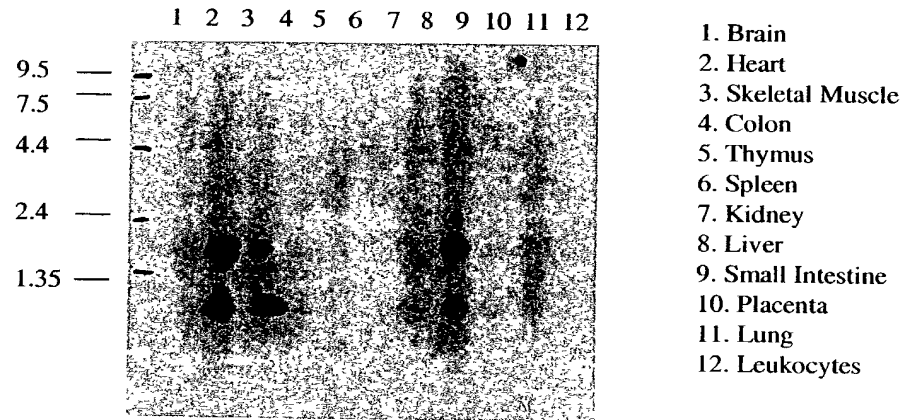


FIG. 6I

Gene 590



Gene 592

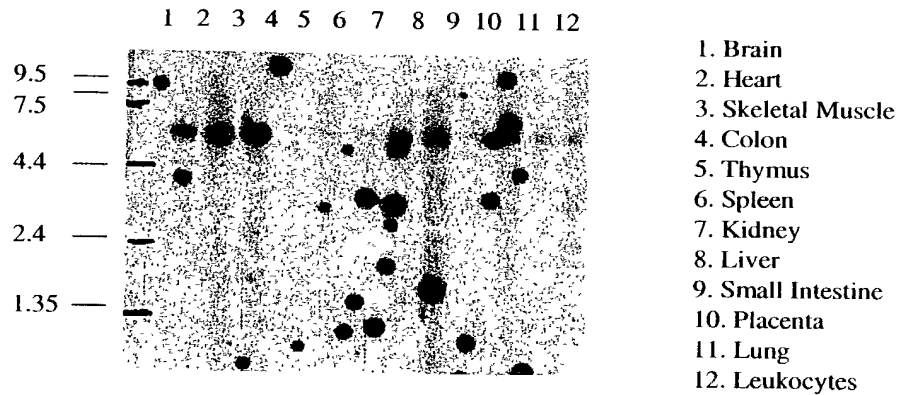
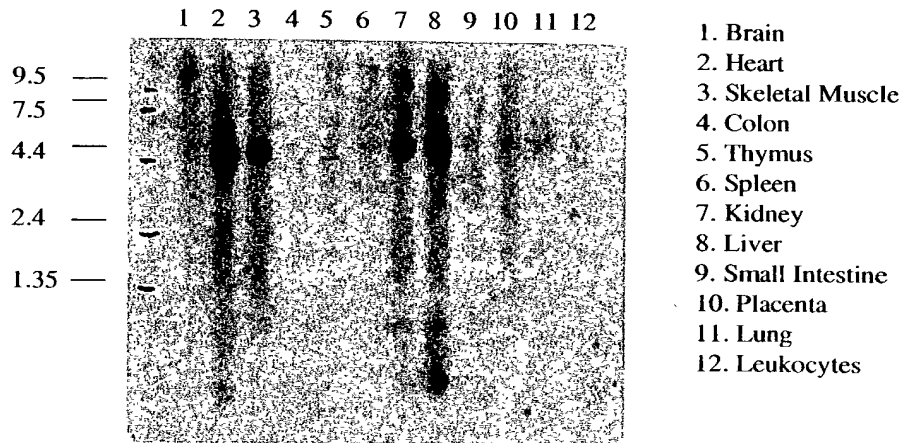


FIG. 6J

Gene 594



Gene 595

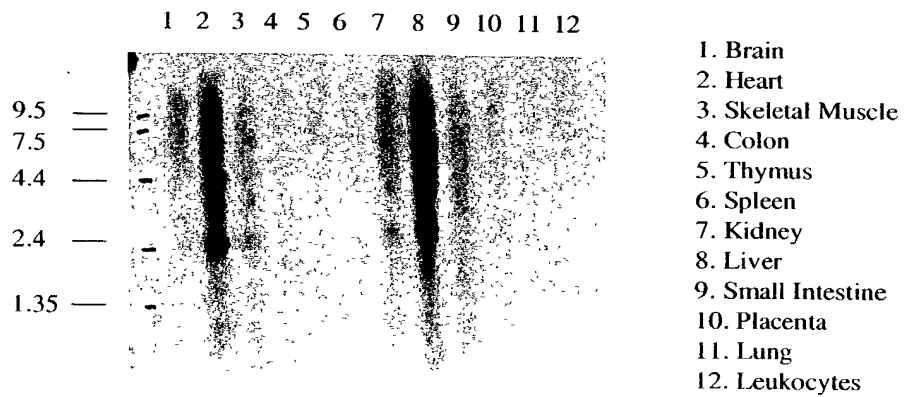
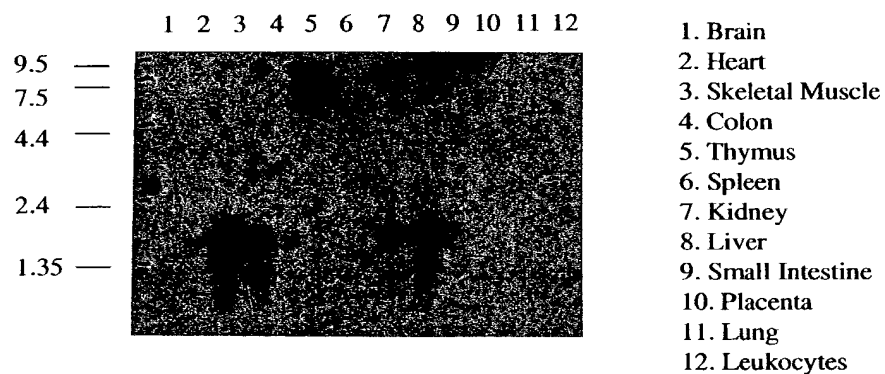


FIG. 6K

[illegible]

Gene 604

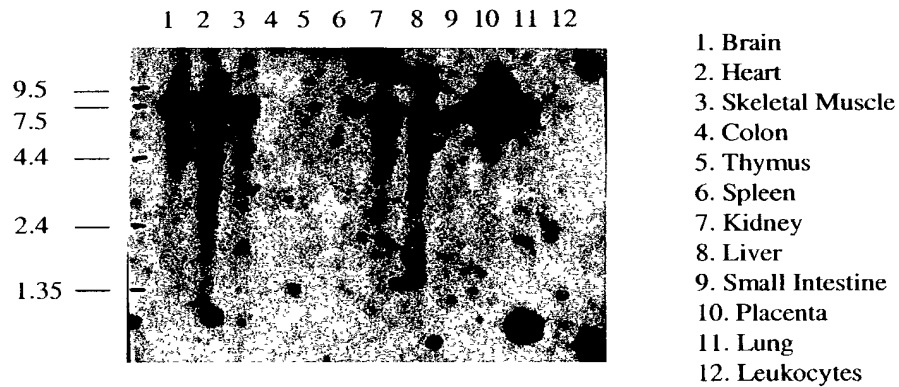
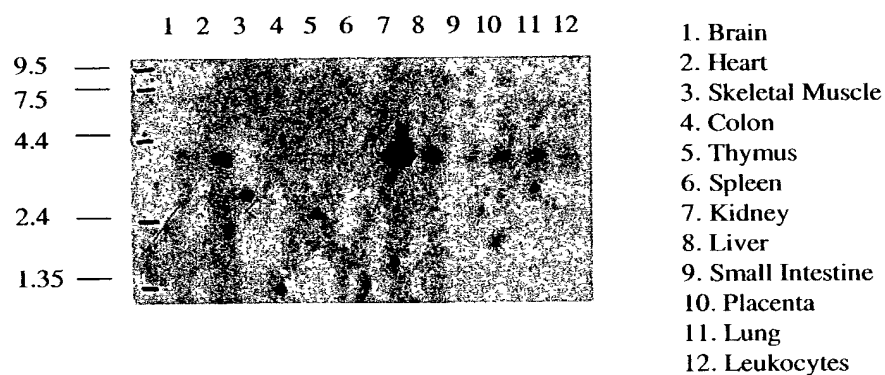


FIG. 6L

Gene 605



Gene 606

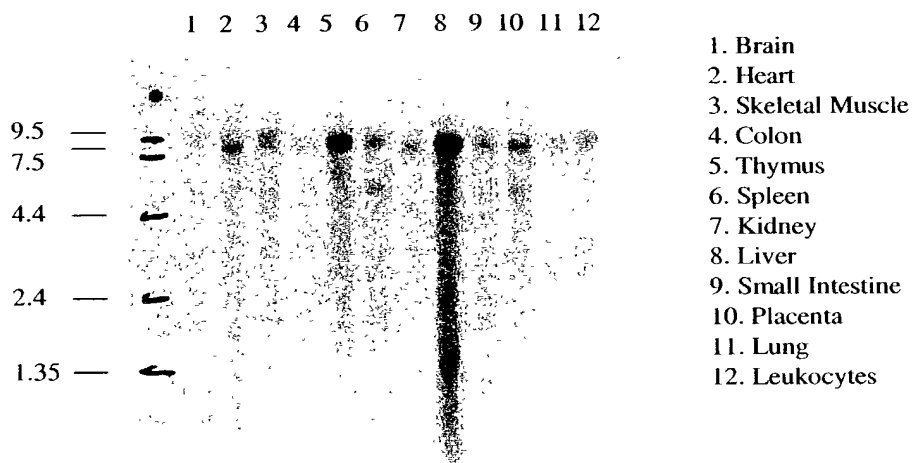
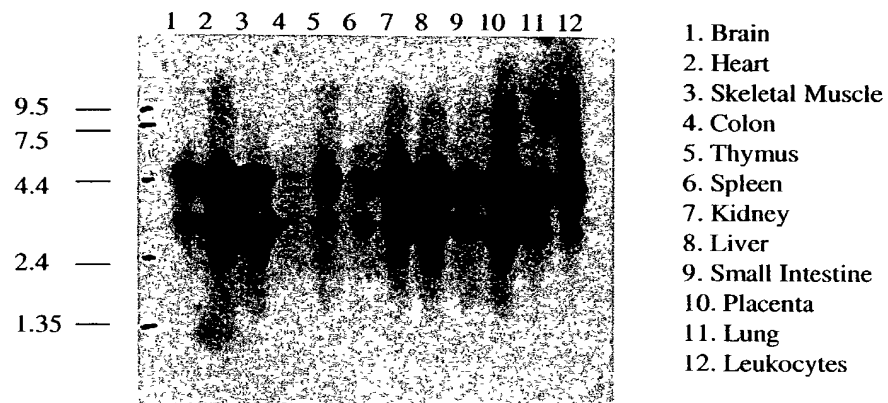


FIG. 6M

Gene 608



Gene 611

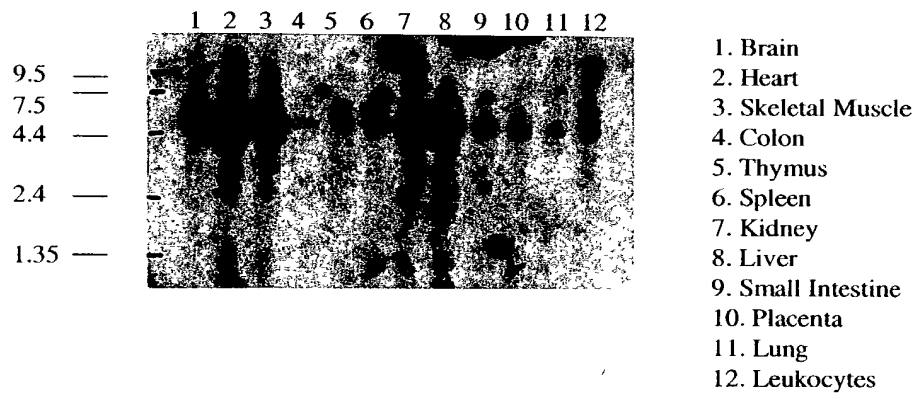


FIG. 6N

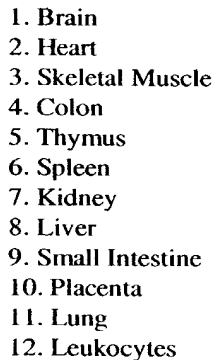
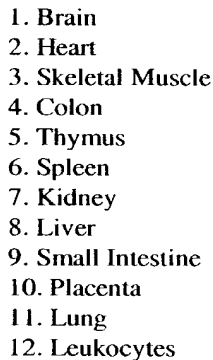
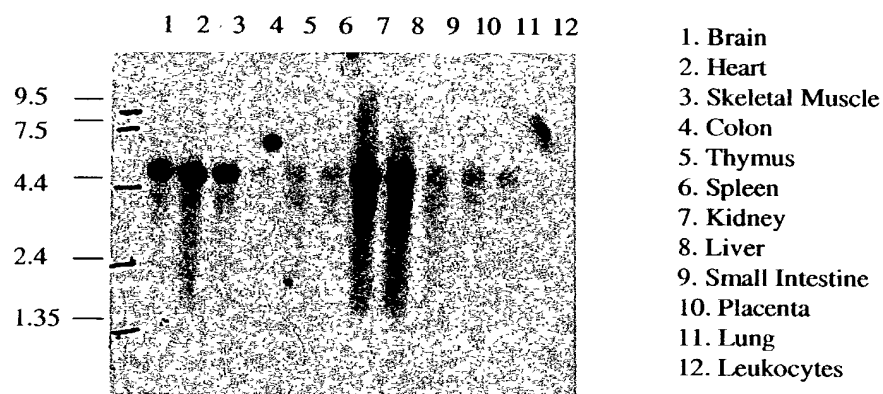
[illegible][illegible]

FIG. 6P

Gene 621



Gene 693

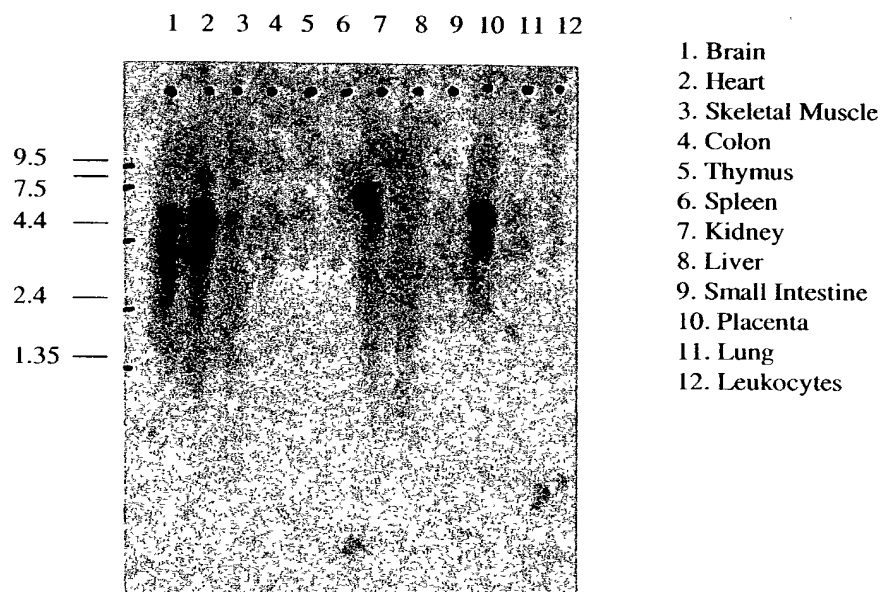
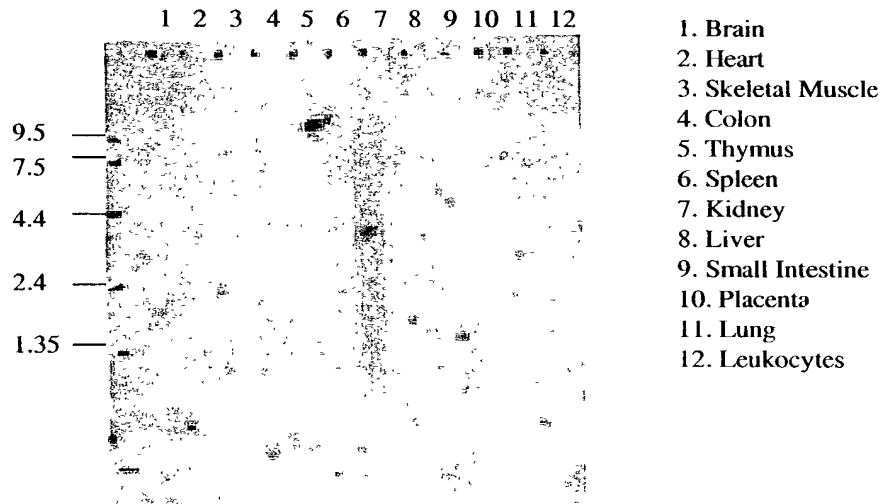


FIG. 6Q

1 2 3 4 5 6 7 8 9 10 11 12

Gene 698



Gene 699

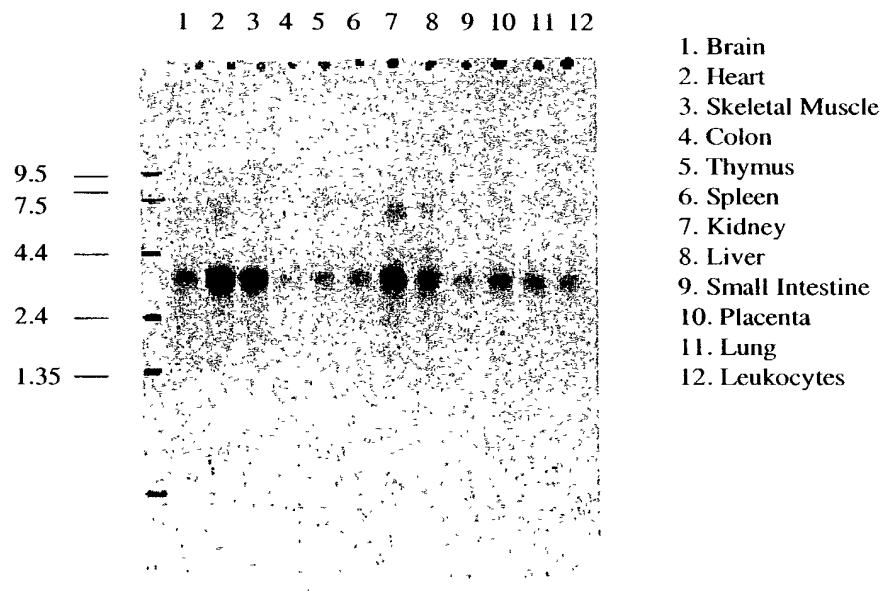


FIG. 6R

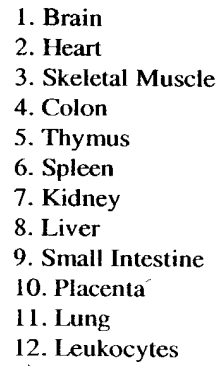
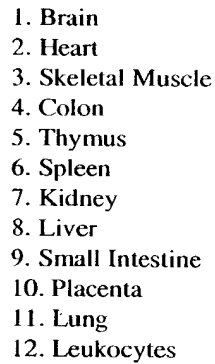
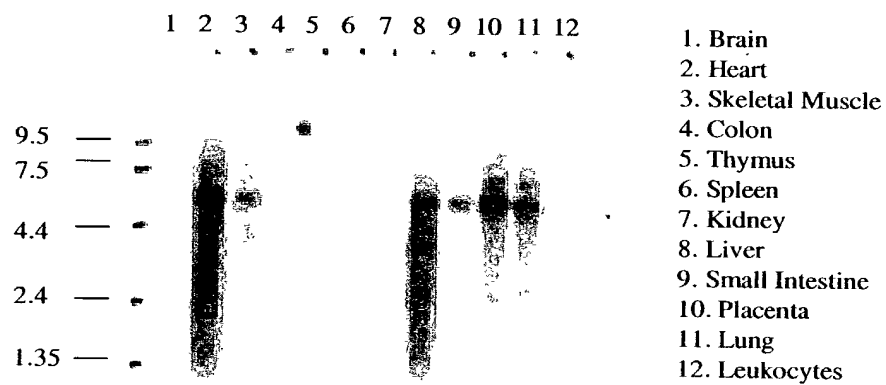
[illegible]

FIG. 6S





Gene 756

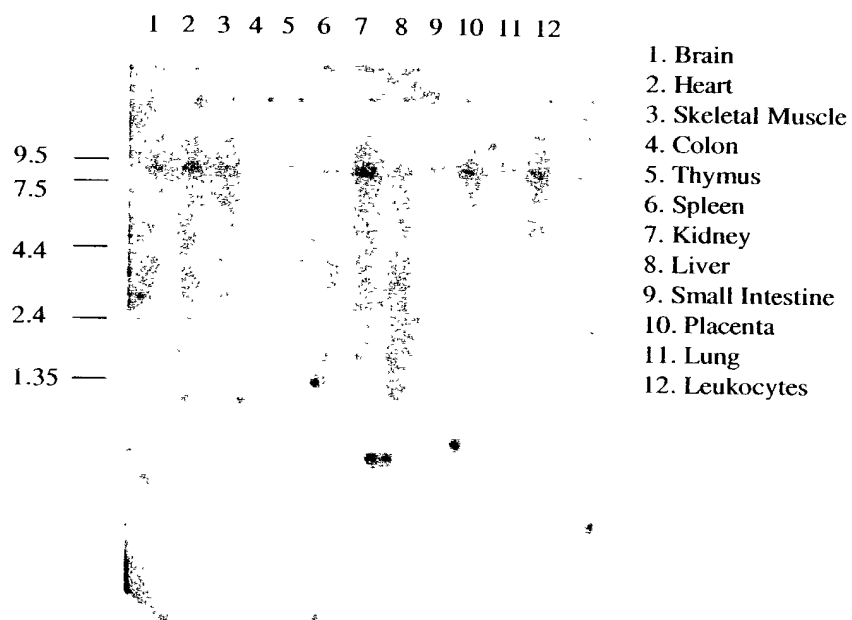


FIG. 6T

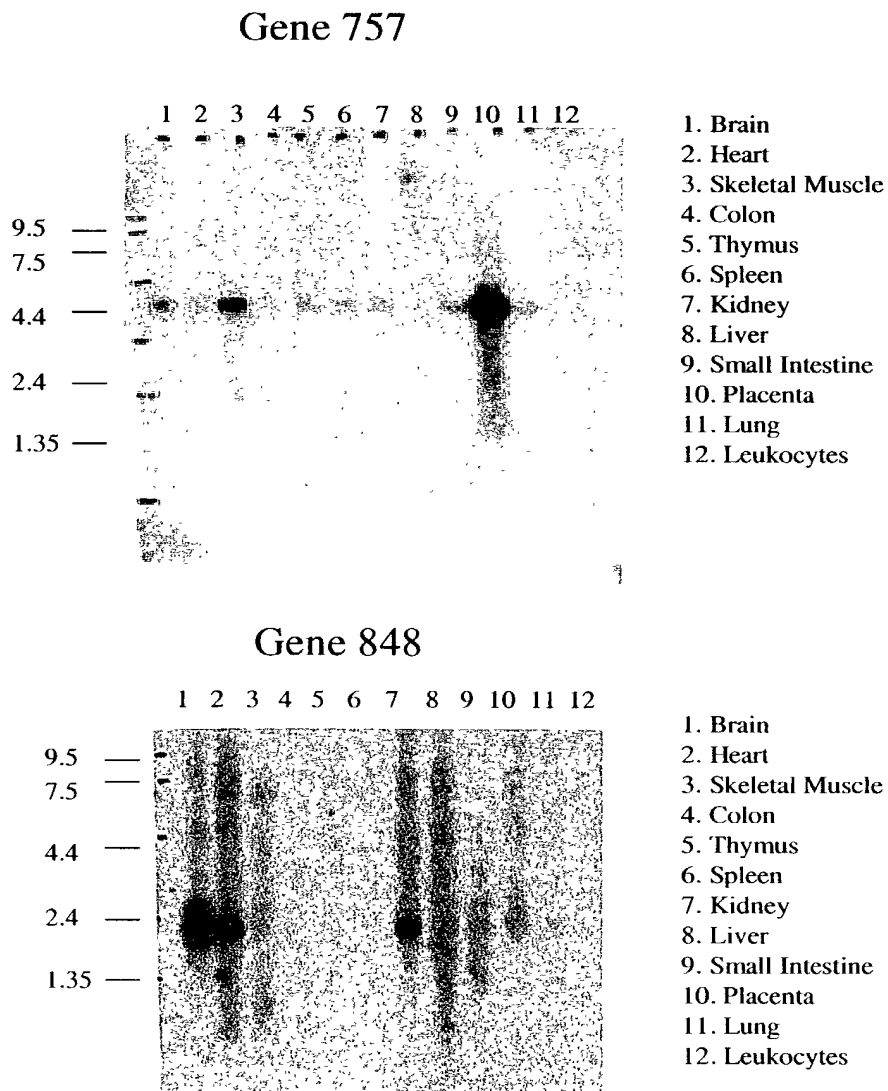


FIG. 6U

10 30 50
GCTTGTCTGTGGCCCTGTCAGGAAGAGTAGAGCTCTGGTCCAGCTCCGCGCAGGGAGGGAG

70 90 110
GCTGTCAACATGCCGGCCTGCTGCAGCTGCAGTGATGTTTTCCAGTATGAGACGAACAAA
MetProAlaCysCysSerCysSerAspValPheGlnTyrGluThrAsnLys

130 150 170
GTCACCTCGGATCCAGAGCATGAATTATGGCACCATTAAAGTGGTTCTTCCACGTGATCATC
ValThrArgIleGlnSerMetAsnTyrGlyThrIleLysTrpPhePheHisValIleIle

190 210 230
TTTTCTACGTTTGCTTTGCTCTGGTGAGTGACAAGCTGTACCAGCGGAAAGAGCCTGTC
PheSerTyrValCysPheAlaLeuValSerAspLysLeuTyrGlnArgLysGluProVal

250 270 290
ATCAGTTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAAGAGGAGATCGTGGAG
IleSerSerValHisThrLysValLysGlyIleAlaGluValLysGluGluIleValGlu

310 330 350
AATGGAGTGAAAGAAGTTGGTGCACAGTGCTTTTGACACCGCAGACTACACCTTCCCTTTG
AsnGlyValLysLysLeuValHisSerValPheAspThrAlaAspTyrThrPheProLeu

370 390 410
CAGGGGAACCTCTTCTTCGTGATGACAAACTTTCTCAAACAGAAGGCCAAGAGCAGCGG
GlnGlyAsnSerPhePheValMetThrAsnPheLeuLysThrGluGlyGlnGluGlnArg

430 450 470
TTGTGTCCCAGATATCCACCCGCAGGACGCTCTGTTCTCTGACCGAGGTTGTAAAAAG
LeuCysProGluTyrProThrArgArgThrLeuCysSerSerAspArgGlyCysLysLys

490 510 530
GGATGGATGGACCCGCAGAGCAAAGGAATTCAGACCCGGAAGGTGTGTAGTGCATGAAGGG
GlyTrpMetAspProGlnSerLysGlyIleGlnThrGlyArgCysValValHisGluGly

550 570 590

AACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGGAAGAGGCCCCC
AsnGlnLysThrCysGluValSerAlaTrpCysProIleGluAlaValGluGluAlaPro

610 630 650
CGGCCTGCTCTCTTGAACAGTGCCGAAAACTCACTGTGCTCATCAAGAACAATATCGAC
ArgProAlaLeuLeuAsnSerAlaGluAsnPheThrValLeuIleLysAsnAsnIleAsp

670 690 710
TTCCCCGGCCACAACCTACACCACGAGAAACATCCTGCCAGGTTTAAACATCACTTGTACC
PheProGlyHisAsnTyrThrThrArgAsnIleLeuProGlyLeuAsnIleThrCysThr

730 750 770
TTCCACAAGACTCAGAATCCACAGTGTCCCATTTTCCGACTAGGAGACATCTTCCGAGAA
PheHisLysThrGlnAsnProGlnCysProIlePheArgLeuGlyAspIlePheArgGlu

790 810 830
ACAGGCGATAATTTTTCAGATGTGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTAC
ThrGlyAspAsnPheSerAspValAlaIleGlnGlyGlyIleMetGlyIleGluIleTyr

850 870 890
TGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCGTCCCAAATACAGTTTCCGTCGC
TrpAspCysAsnLeuAspArgTrpPheHisHisCysArgProLysTyrSerPheArgArg

910 930 950
CTTGACGACAAGACCACCAACGTGTCTTGTACCCTGGCTACAACCTTCAGATACGCCAAG
LeuAspAspLysThrThrAsnValSerLeuTyrProGlyTyrAsnPheArgTyrAlaLys

970 990 1010
TACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTTCGGGATCCGTTTT
TyrTyrLysGluAsnAsnValGluLysArgThrLeuIleLysValPheGlyIleArgPhe

1030 1050 1070
GACATCCTGGTTTTTGGCACCGGAGGAAAATTGACATTATCCAGCTGGTTGTGTACATC
AspIleLeuValPheGlyThrGlyGlyLysPheAspIleIleGlnLeuValValTyrIle

1090 1110 1130
GGCTCAACCCTCTCCTACTTCCGGTCTGGCCACTGTGTTTCATCGACTTCCTCATCGACACT
GlySerThrLeuSerTyrPheGlyLeuAlaThrValPheIleAspPheLeuIleAspThr

FIG. 7B

1150 1170 1190
TACTCCAGTAACTGCTGTCGCTCCCATATTTATCCCTGGTGCAAGTGCTGTCAGCCCTGT
TyrSerSerAsnCysCysArgSerHisIleTyrProTrpCysLysCysCysGlnProCys

1210 1230 1250
GTGGTCAACGAATACTACTACAGGAAGAAGTGCGAGTCCATTGTGGAGCCAAAGCCGACA
ValValAsnGluTyrTyrTyrArgLysLysCysGluSerIleValGluProLysProThr

1270 1290 1310
TTAAAGTATGTGTCCTTTGTGGATGAATCCCACATTAGGATGGTGAACCAGCAGCTACTA
LeuLysTyrValSerPheValAspGluSerHisIleArgMetValAsnGlnGlnLeuLeu

1330 1350 1370
GGGAGAAGTTTGCAAGATGTCAAGGGCCAAGAAGTCCCAAGACCTGCGATGGACTTCACA
GlyArgSerLeuGlnAspValLysGlyGlnGluValProArgProAlaMetAspPheThr

1390 1410 1430
GATTTGTCCAGGCTGCCCCCTGGCCCTCCATGACACACCCCGATTCTGGACAACCAGAG
AspLeuSerArgLeuProLeuAlaLeuHisAspThrProProIleProGlyGlnProGlu

1450 1470 1490
GAGATACAGCTGCTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAGCCCCGTCTGGTGC
GluIleGlnLeuLeuArgLysGluAlaThrProArgSerArgAspSerProValTrpCys

1510 1530 1550
CAGTGTGGAAGATGCCTCCCATCTCAACTCCCTGAGAGCCACAGGTGCCTGGAGGAGCTG
GlnCysGlyArgCysLeuProSerGlnLeuProGluSerHisArgCysLeuGluGluLeu

1570 1590 1610
TGCTGCCGGAAGCCGGGGCCTGCATCACCACCTCAGAGCTGTTACAGGAAGCTGGTC
CysCysArgLysLysProGlyAlaCysIleThrThrSerGluLeuPheArgLysLeuVal

1630 1650 1670
CTGTCCAGACACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGCCCTTGCTGGCGCTGGAT
LeuSerArgHisValLeuGlnPheLeuLeuLeuTyrGlnGluProLeuLeuAlaLeuAsp

1690 1710 1730

FIG. 7C

GTGGATTCCACCAACAGCCGGCTGCGGCACTGTGCCTACAGGTGCTACGCCACCTGGCGC
ValAspSerThrAsnSerArgLeuArgHisCysAlaTyrArgCysTyrAlaThrTrpArg

1750 1770 1790
TTCGGCTCCCAGGACATGGCTGACTTTGCCATCCTGCCCAGCTGCTGCCGCTGGAGGATC
PheGlySerGlnAspMetAlaAspPheAlaIleLeuProSerCysCysArgTrpArgIle

1810 1830 1850
CGGAAAGAGTTTCCAAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAGTCCTTACTGAAGC
ArgLysGluPheProLysSerGluGlyGlnTyrSerGlyPheLysSerProTyrEnd

1870 1890 1910
CAGGCACCGTGGCTCACGTCTGTAATCCCAGCGCTTTGGGAGGCCGAGGCAGGCAGATCA

1930 1950 1970
CCTGAGATCGGGAGTTGGAGACCCGCCTGGCTAACAAGGCGAAATCCTGTCTGTACTAAA

1990 2010 2030
AATACAAAATCAGCCAGACATGGTGGCATGCACCTGCAATCCCAGCTACTCGGGAGGCT

2050 2070 2090
GAGGCACAAGAATCACTTGAACCCGGGAGGCAGAGGTTGTAGTGAGCCCAGATTGTGCCA

2110 2130 2150
CTGCTCTCCAGCCTGGGAGGCACAGCAAACGTGCCAAAAAAAAAAAAAAAAAGAGTCCTTAC

2170 2190 2210
CAATAGCAGGGGCTGCAGTAGCCATGTTAAACATGACATTTACCAGCAACTTGAACCTCAC

2230 2250 2270
CTGCAAAGCTCTGTGGCCACATTTTCAGCCAAAGGGAATATGCTTTTCATCTTCTGTTGC

2290 2310 2330
TCTCTGTGTCTGAGAGCAAAGTGACCTGGTTAAACAAACCAGAATCCCTCTACATGGACT

2350 2370 2390

FIG. 7D

CAGAGAAAAGAGATTGAGATGTAAGTCTCAACTCTGTCCCCAGGAAGTTGTGTGACCCTA

2410 2430 2450

GGCCTCTCACCTCTGTGCCTCTGTCTCCTTGTGGCCAACTACTATCTCAGAGATATTGT

2470 2490 2510

GAGGACAAATTGAGACAGTGCACATGAACGTCTTTTAATGTGTAAAGATCTACATGAAT

2530 2550 2570

GCAAAACATTTTATTATGAGGTGAGACTAGGATAATGTCCAACTAAAAACAAACCCTTTT

2590 2610 2630

CATCCTGGCTGGAGAATGTGGAGAACTAAAGGTGGCCACAAATTCTTTGACACTCAAGTC

2650 2670 2690

CCCCAAGACCTAAGGGTTTTATCTCCTCCCCTTGAATATGGGTGGCTCTGATTGCTTTAT

2710 2730 2750

CCAAAAGTGGAAGTGACATTGTGTGAGTTTTCAGATCCTGATCTTAAGAGGCTGACAGCTT

2770 2790 2810

CTACTTGCTGTCCCTTGGAACTCTTGCTATCGGGGAAGCCAGACGCCATTTAAAGTCTG

2830 2850 2870

CCTATCCTGGCCAGGTGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGACCAAGG

2890 2910 2930

CGGGCGGATCACTTAAAGTCAGGAGTCCAAGACCAGACTCGCCAACATGGTGAAACCGTA

2950 2970 2990

TCTCTAATAAAAAATACAAAAATTAGCTGGGCATGGTGCGGGCACCTGTAGTCTTAGCTAT

3010 3030 3050

CAAGAGGCTGAGACAGGAGAAACACTTGAACCTGGGAGGTGGAGGTTGCATTGAGCTGAG

FIG. 7E

3070 3090 3110
 ATCGTGCCACTGCACTCCAGGCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAAAAA

3130 3150 3170
 AAAAGAAAAAAAAATGTCTGCCTATCCTGAGACTGCCCTGCTGTGAGGAAGCCCAAGCA

3190 3210 3230
 GTCACGTGGACAGTGCCTGACCAGCCCCAGCTTTCAAGCCATCCAAGCCCAGTCACCAA

3250 3270 3290
 CATGAGAGAGAAGAAGCCTTCAGGTGATTCTGGACTCCACTAACATATGACTGATACCGC

3310 3330 3350
 ATGATACATCCCAAGTGAGAACTGCCCCATAAATCCAGAAAACCACATTGCTATCTTAAG

3370 3390 3410
 TCCCTAAGTTTGGGGCTTATTTGTTCCACAGCAACAGGTAAGTGAACAGAGGGCAAGCC

3430 3450 3470
 TGATGAATGGGCACACAGACTCAGCCCATACTTCCCTGGTTCTAATGTTCTCAGGGAGC

3490 3510 3530
 CCGGACCAACCCTGGGAGCCTCAGGAAGTTAGGTTTCCACTGGACAGTTCTAGAAGGGCT

3550 3570 3590
 ATAGACCAAATCAGGTAAGTACCAGACCAGCCTTGAATCTATCAAATCTAACTGCTGA

3610 3630 3650
 GCTACCCAGTGCATTCCGATCCTCATCACAATTCTTTGACTGAAGGCCGGGCGTGGTGGC

3670 3690 3710
 TCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCCGGTGGATCACCTGAGGTCAGGA

FIG. 7F

3730 3750 3770
 GTTCGAGACCAGCCTGGCCAAACATGGTGAGACCCTGTCTCTACTAAGAATACAAAAATTA
 3790 3810 3830
 GGTGGGGTGGCGGTGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATC
 3850 3870 3890
 TCTTGAACCTGGAAGGTGGAGGTTGCAATAAGCCGAGATAGTGCCACTGCACTCCAGCCT
 3910 3930 3950
 AGATAACAGAGCAAGACTCTGTCTCAAAAAACAACAACAACAACAACAATTCAT
 3970 3990 4010
 GACTGAAAGTGACTAAAAAGCTGGCTTTATGCCATTAACACTCTGTACTTTGCAGCCAAT
 4030 4050 4070
 CAGAACTGACGCAGTCTGGGTGCTAGCTGCTTCAAAAGCAACCCACACCACACTTTTACC
 4090 4110 4130
 ATTTCCATACATCAACTGCTGAGAATATGAAAATGCACAGTGACAGGTTTTAGGATCCTG
 4150 4170 4190
 CTCAGGATTTTCCTTTTCCCTGGTTGGTCACTAGAGTTGGCTATTTATCTGTTTCTAAAC
 4210 4230 4250
 AATAGCTATTTTATCGAATAGTTTAGAGACCACTATTAAATATTGTGACTGATGAAGGAT
 4270 4290 4310
 CTGTGAATTTTTTTATATATGTTCTAAGAGTTACCATTTTGATACCTTTTAAAAACCAGC
 4330 4350 4370
 AGCTTTCTACTATATTCATGTAAAACAGCATGAATAAAACCATTTTTTGATACAGGGTTT
 4390 4410 4430

FIG. 7G

TATTTGGCTTTAAACTCAGGAACCAAGTTAATTATGCCAGATTGAACTTTGATTTTTACT

4450

4470

4490

ACCTTTTCAAAGATATTTTAAAAAGTGGATTACTACATATGATTTCTTTGGAGCTTACAT

4510

4530

4550

TTCTTTACTTCACGAATTCTATGTCACGTGTTACAAGTTCCATTCTGATGGCTTCTGGGC

4570

4590

4610

CTTTGTACCTTTGTTTTTGGTGCCTTATTCCTAGTATGTTTCTATCACCTTAATGAGGCC

4630

4650

4670

GCAGATGGAGTCAGAATGTGAAATTACAAATAATCACTGGATCCATCTACTGTTTTCCAT

4690

4710

4730

CACCTTCCCCACTGATGCTCTGGGCGAGAGAGTGATGTGTCACTTCACTGTGTGTAATA

4750

4770

4790

TGTCAGACACGTCCTACAATAACAGGCGTCATATTTGTATTATTTTTAGTTTACTGTAGA

4810

4830

4850

AAATAATGTCAACGCCAAAGGTGATGAGAGTCACGTTTTGTAGGATCTGTTTTCTTATAC

4870

4890

4910

TTAAAGACAGACTTCTGCTACGGTAATTGCCAGTATTCATGGCTTCCTTTCTGTGTCAGA

4930

4950

4970

AGAGAAGGGATCTGCTTTCTCTGGCTGATTTACATAGCATTGGTAATAGACATGCATT

4990

5010

5030

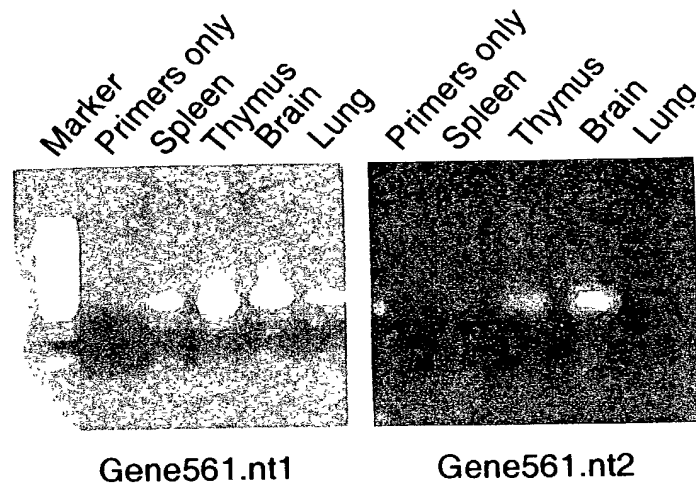
TCTCTTTCTAAAGGGGAGTAACTTTTTAAACCTTCCTGATTTTAGCCTGGCAATGTAAG

5050

5070

TGTCCTTAATGTGACTGTTTTGATAATTAATAAAGGTATATAATTT

FIG. 7H



RT/PCR of Gene561.nt1 and Gene561.nt2

FIG. 8

10 30 50
TCGAAACAGCTGCCGGCTGGTCCCGGCCGAGGCCGGCGCAGGGAGGGAGGAGCCGCCCGG

70 90 110
GCTGTGGGGGCGCCGCGAGCTGGGCCGGCCTCGGTGTGCCCGCGCCGCCAGCCCGCTCCA

130 150 170
GACGCGCCACCTGGGCGCTCCAAGAAGAGGCCGAAGTTTGCCGCGGCCGTGAGTTGGAGC

190 210 230
TCGCGCCGGGCGCTGCGCCGGGAGCTCCGGGGGCTTCCCTCGCTTCCCGGTATTGTTTG

250 270 290
CAAACCTTGCTGCTCTCCGCCGCGGCCCCCAACTCGGCGGACGCCGGGCGCGGAGAGCCG

310 330 350
AGCCGGGGGCGCTGTGCGCAGCGCTCGGGCCAGGCCGGGCGGGCATGGGCGGGGGCCCCGA

370 390 410
GCAGGGGTGGAGAGCCGGGGCCAGCAGCAGCCCGTGCCCGGGAGCGGCGGCGCTGAGGGG

430 450 470
CGCGGAGCTCCCCGCGAGGACACGTCCAACGCCAGCATGCAGCGCCCGGGCCCCCGCTG
MetGlnArgProGlyProArgLeu

490 510 530
TGGCTGGTCCTGCAGGTGATGGGCTCGTGCGCCGCCATCAGCTCCATGGACATGGAGCGC
TrpLeuValLeuGlnValMetGlySerCysAlaAlaIleSerSerMetAspMetGluArg

550 570 590
CCGGGCGACGGCAAATGCCAGCCCATCGAGATCCCGATGTGCAAGGACATCGGCTACAAC
ProGlyAspGlyLysCysGlnProIleGluIleProMetCysLysAspIleGlyTyrAsn

610 630 650

FIG. 9A

ATGACTCGTATGCCCAACCTGATGGGCCACGAGAACCAGCGCGAGGCAGCCATCCAGTTG
MetThrArgMetProAsnLeuMetGlyHisGluAsnGlnArgGluAlaAlaIleGlnLeu

670 690 710
CACGAGTTCGCGCCGCTGGTGGAGTACGGCTGCCACGGCCACCTCCGCTTCTTCCTGTGC
HisGluPheAlaProLeuValGluTyrGlyCysHisGlyHisLeuArgPhePheLeuCys

730 750 770
TCGCTGTACGCGCCGATGTGCACCGAGCAGGTCTCTACCCCCATCCCCGCTGCCGGGTC
SerLeuTyrAlaProMetCysThrGluGlnValSerThrProIleProAlaCysArgVal

790 810 830
ATGTGCGAGCAGGCCCGGCTCAAGTGCTCCCGATTATGGAGCAGTTCAACTTCAAGTGG
MetCysGluGlnAlaArgLeuLysCysSerProIleMetGluGlnPheAsnPheLysTrp

850 870 890
CCCGACTCCCTGGACTGCCGGAACCTCCCCAACAAGAACGACCCCACTACCTGTGCATG
ProAspSerLeuAspCysArgLysLeuProAsnLysAsnAspProAsnTyrLeuCysMet

910 930 950
GAGGCGCCCCAACACGGCTCGGACGAGCCCACCCGGGGCTCGGGCCTGTTCCCGCCGCTG
GluAlaProAsnAsnGlySerAspGluProThrArgGlySerGlyLeuPheProProLeu

970 990 1010
TTCCGGCCGCAGCGGCCCCACAGCGCGCAGGAGCACCCTGAAGGACGGGGGCCCGGG
PheArgProGlnArgProHisSerAlaGlnGluHisProLeuLysAspGlyGlyProGly

1030 1050 1070
CGCGGCGGCTGCGACAACCCGGGCAAGTTCCACCACGTGGAGAAGAGCGCGTCGTGCGCG
ArgGlyGlyCysAspAsnProGlyLysPheHisHisValGluLysSerAlaSerCysAla

1090 1110 1130
CCGCTCTGCACGCCCGGCGTGGACGTGTACTGGAGCCGCGAGGACAAGCGCTTCGCAGTG
ProLeuCysThrProGlyValAspValTyrTrpSerArgGluAspLysArgPheAlaVal

1150 1170 1190

FIG. 9B

$$\begin{aligned} & \frac{\partial^2 u}{\partial x^2} + \frac{\partial^2 v}{\partial y^2} = \frac{\partial^2 w}{\partial z^2} \\ & \frac{\partial^2 u}{\partial x^2} + \frac{\partial^2 v}{\partial y^2} = \frac{\partial^2 w}{\partial z^2} \end{aligned}$$

1

$$-\frac{d^2}{dt^2} \left(\frac{\partial L}{\partial \dot{x}} \right) + \frac{\partial L}{\partial x} = 0, \quad -\frac{d^2}{dt^2} \left(\frac{\partial L}{\partial \dot{y}} \right) + \frac{\partial L}{\partial y} = 0, \quad -\frac{d^2}{dt^2} \left(\frac{\partial L}{\partial \dot{z}} \right) + \frac{\partial L}{\partial z} = 0,$$

1790

100

1850

100

1910

100

1970

100

2030

100

2090

100

2150

100

2210

100

2270

$$\frac{1}{\Gamma(\alpha)} \int_0^t (t-\tau)^{\alpha-1} f(\tau) d\tau = I^\alpha f(t), \quad t \geq 0, \quad (1)$$

100

2950 2970 2990

TACATTTTGTGGCTTTTAAATGGAAACCAAGCCAATGTTATAGACGTTTGGACTGATTTG

3070 3090 3110
CTCTTCTATTGTTAAACAAATGATTTCACAAACAGATCAGGAAGCACTAGGTTGGCAG

3190 3210 3230
ATATTTGTAATATATGATATTTTTCATGCTCCACTATTTTATTA AAAATATAATATGTTCT

FIG. 9F

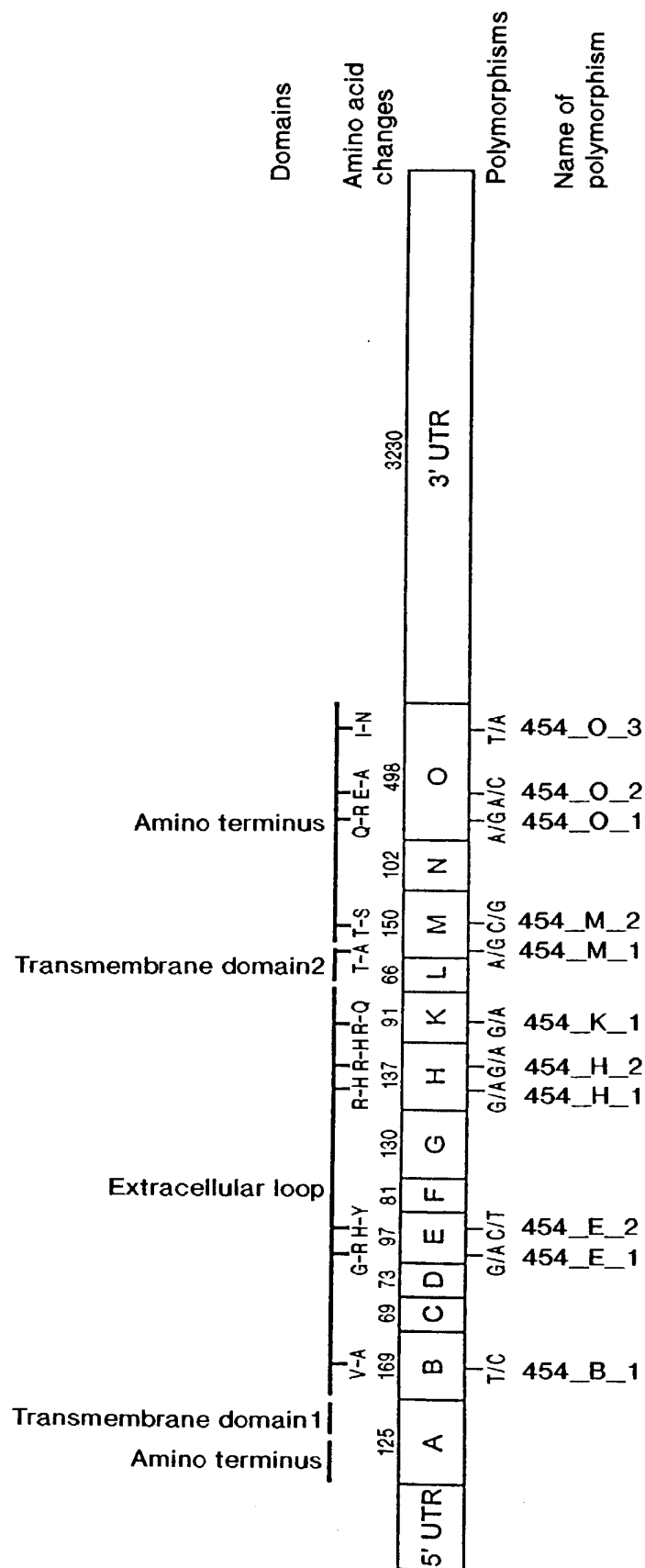


FIG. 10

Chr. 12 Case(Asthma)/Control: Alleles

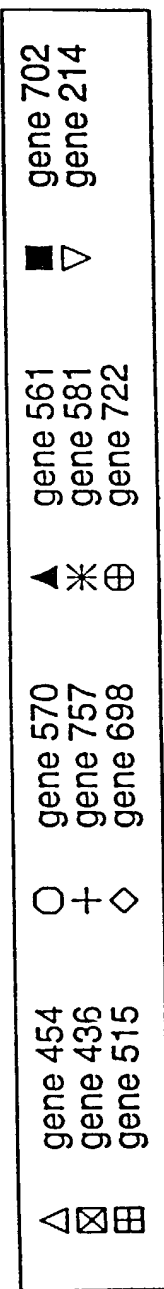
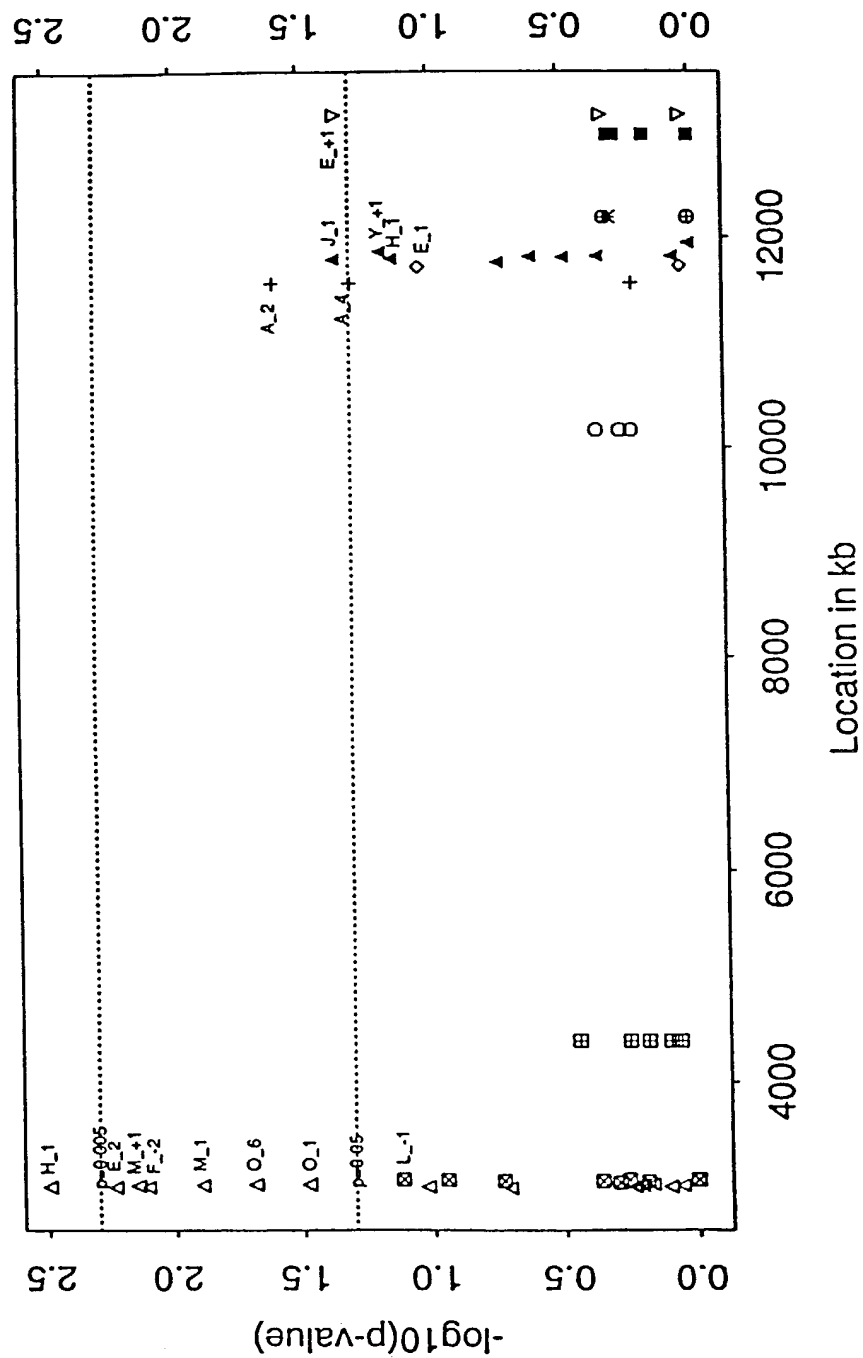


FIG. 11

Chr. 12 Case(Asthma)/Control: Alleles

US

UK

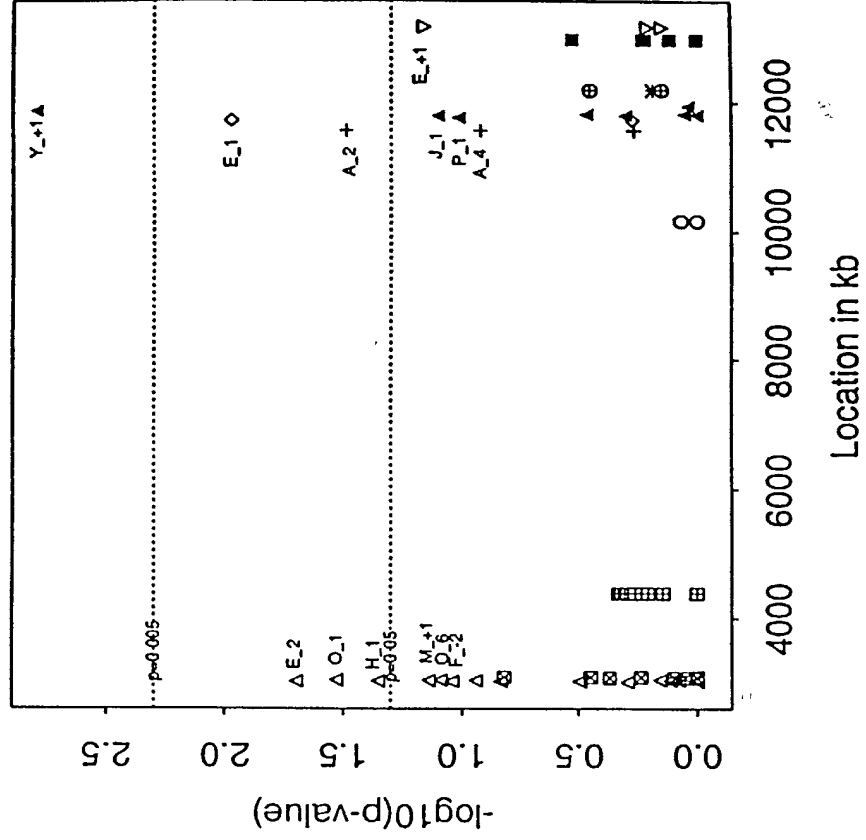
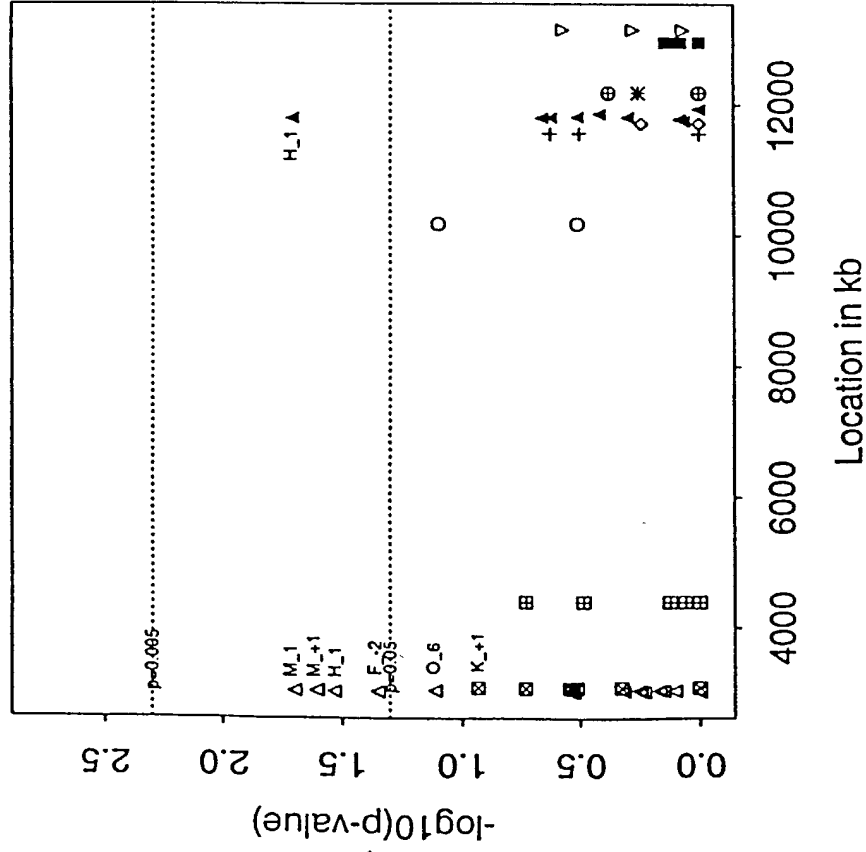


FIG. 12

Δ	gene 454	\square	gene 561	\blacksquare	gene 702
\boxtimes	gene 436	$+$	gene 570	\blacktriangle	gene 214
\boxplus	gene 515	\diamond	gene 757	\ast	gene 581
			gene 698	\oplus	gene 722

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Alleles

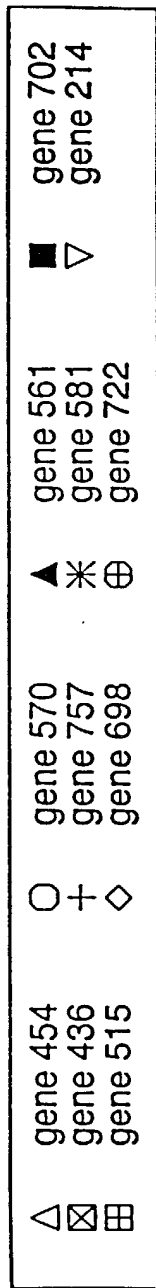
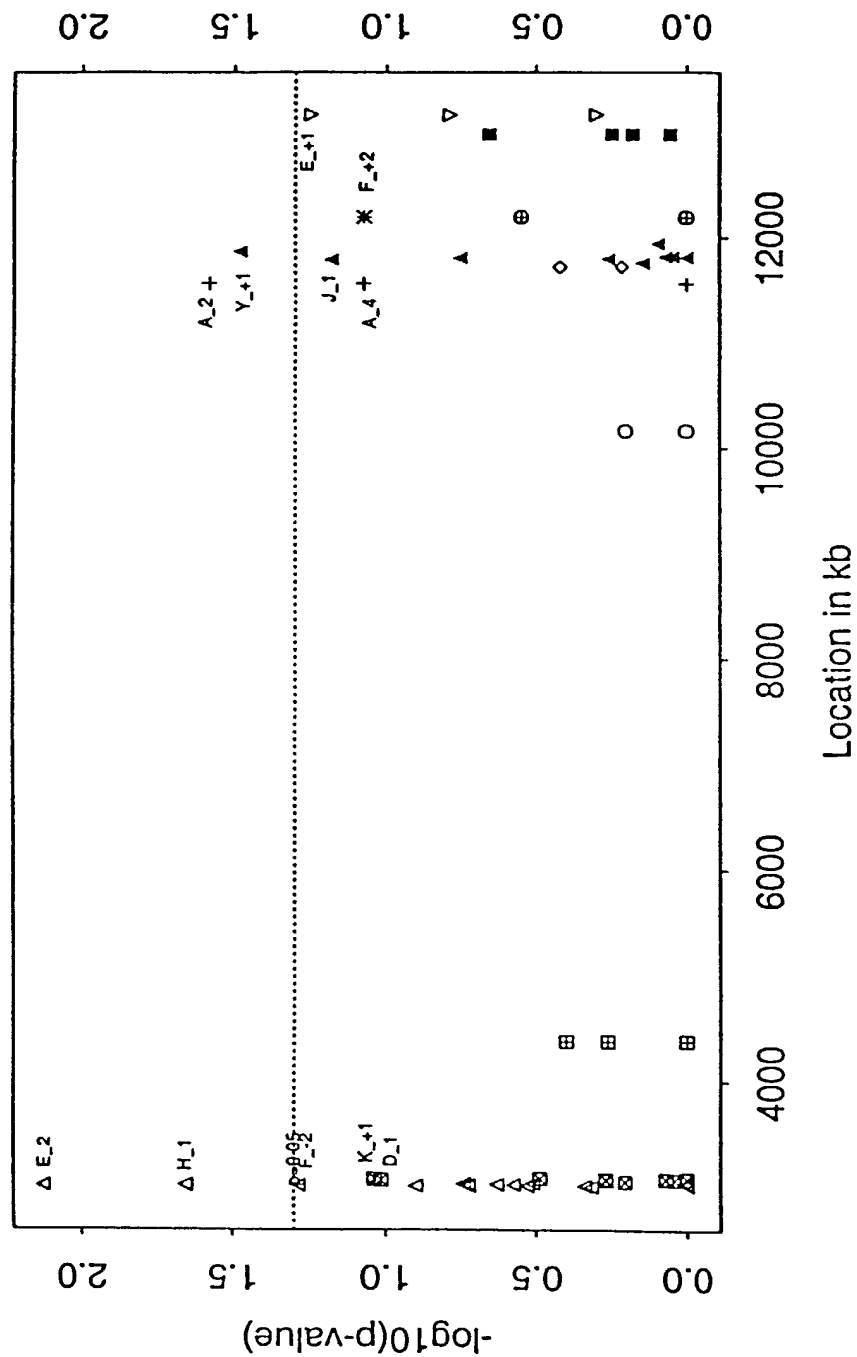


FIG. 13

Chr. 12 Case(BHR (PC20 \leq 16 mg/ml) & Asthma)/Control: Alleles

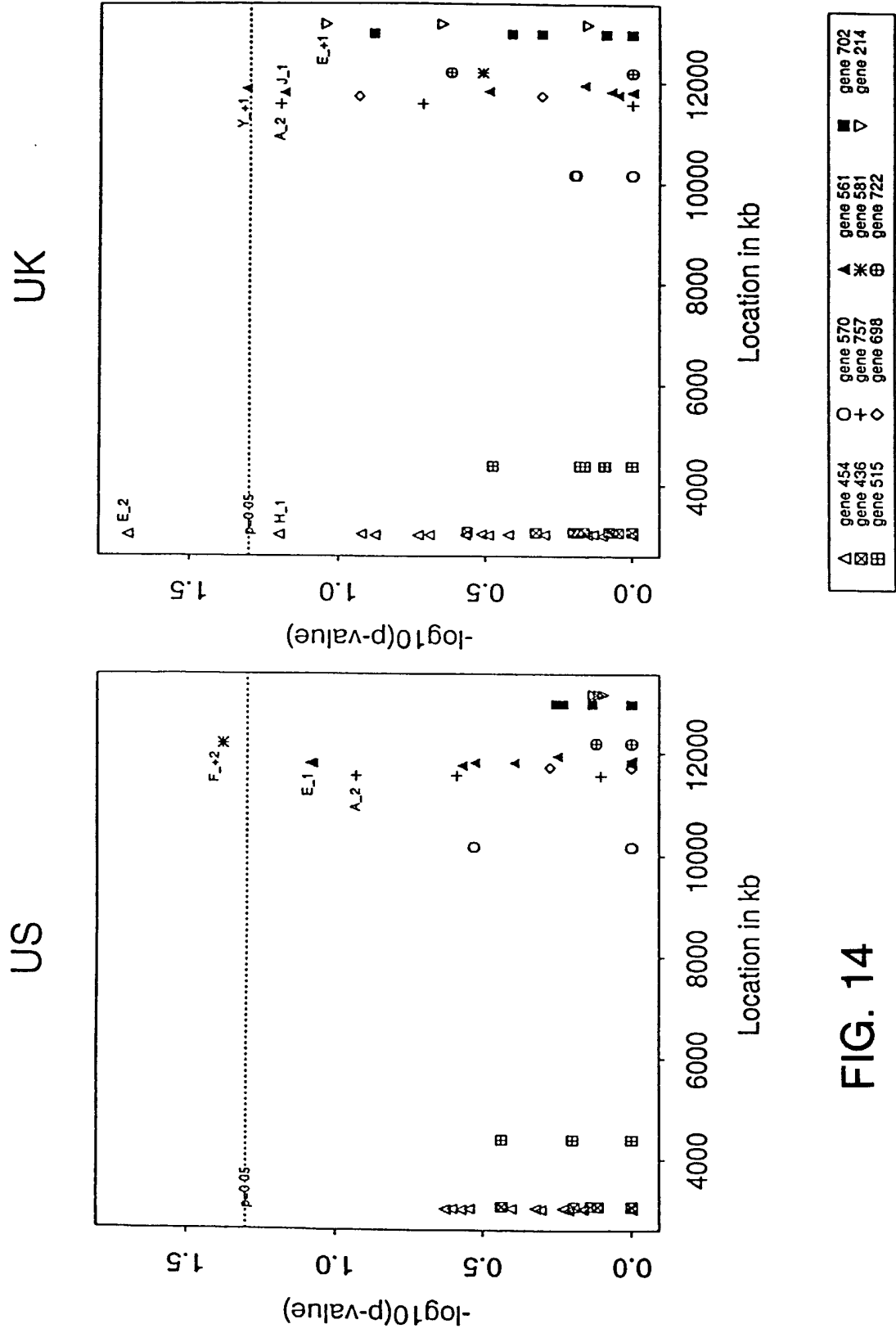


FIG. 14

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

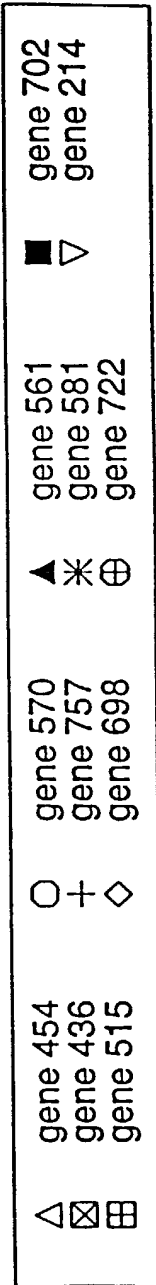
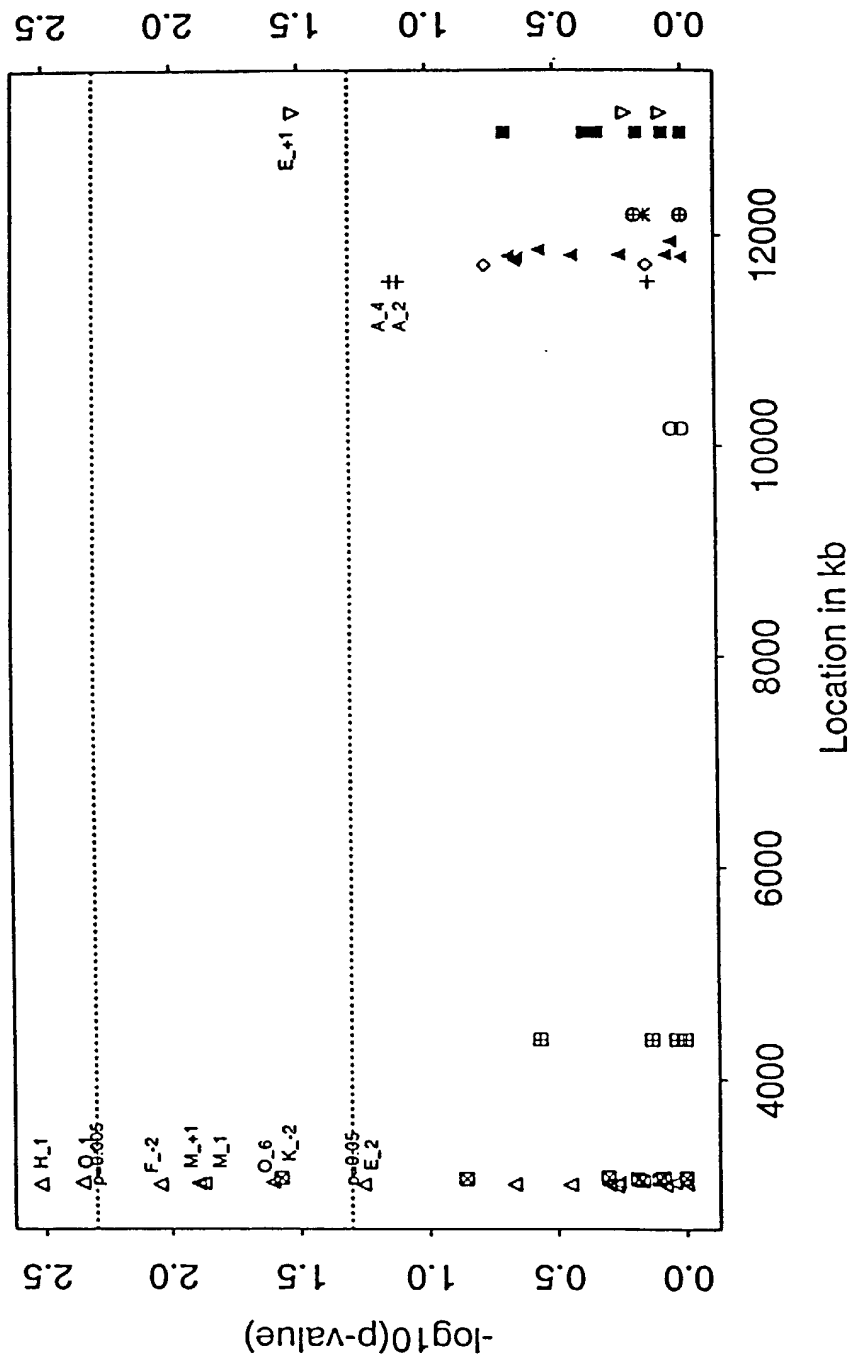
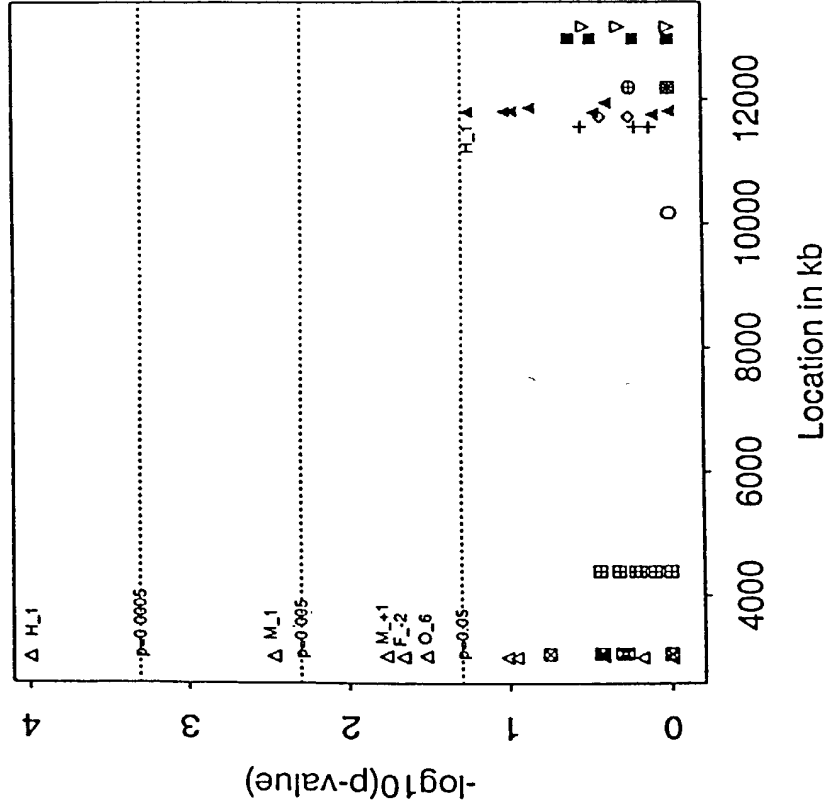


FIG. 15

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

US



UK

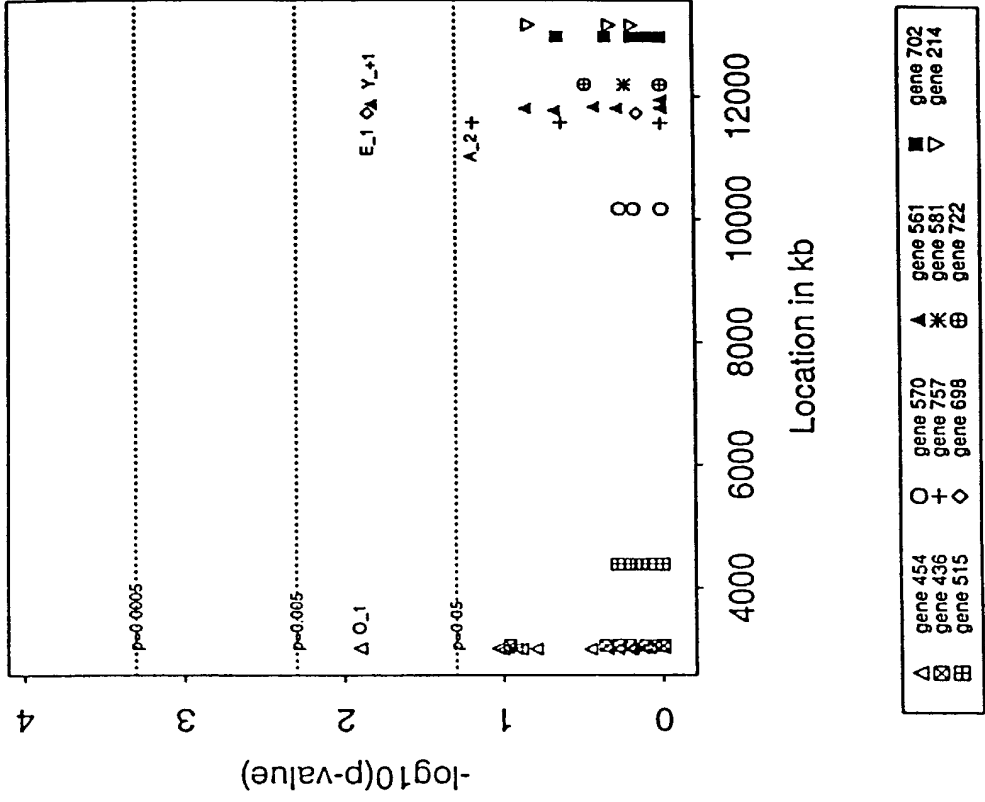


FIG. 16

Δ	gene 454	\circ	gene 570	\blacktriangle	gene 561	\blacksquare	gene 702
\boxtimes	gene 436	$+$	gene 757	\ast	gene 581	∇	gene 214
\boxplus	gene 515	\diamond	gene 698	\oplus	gene 722		

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

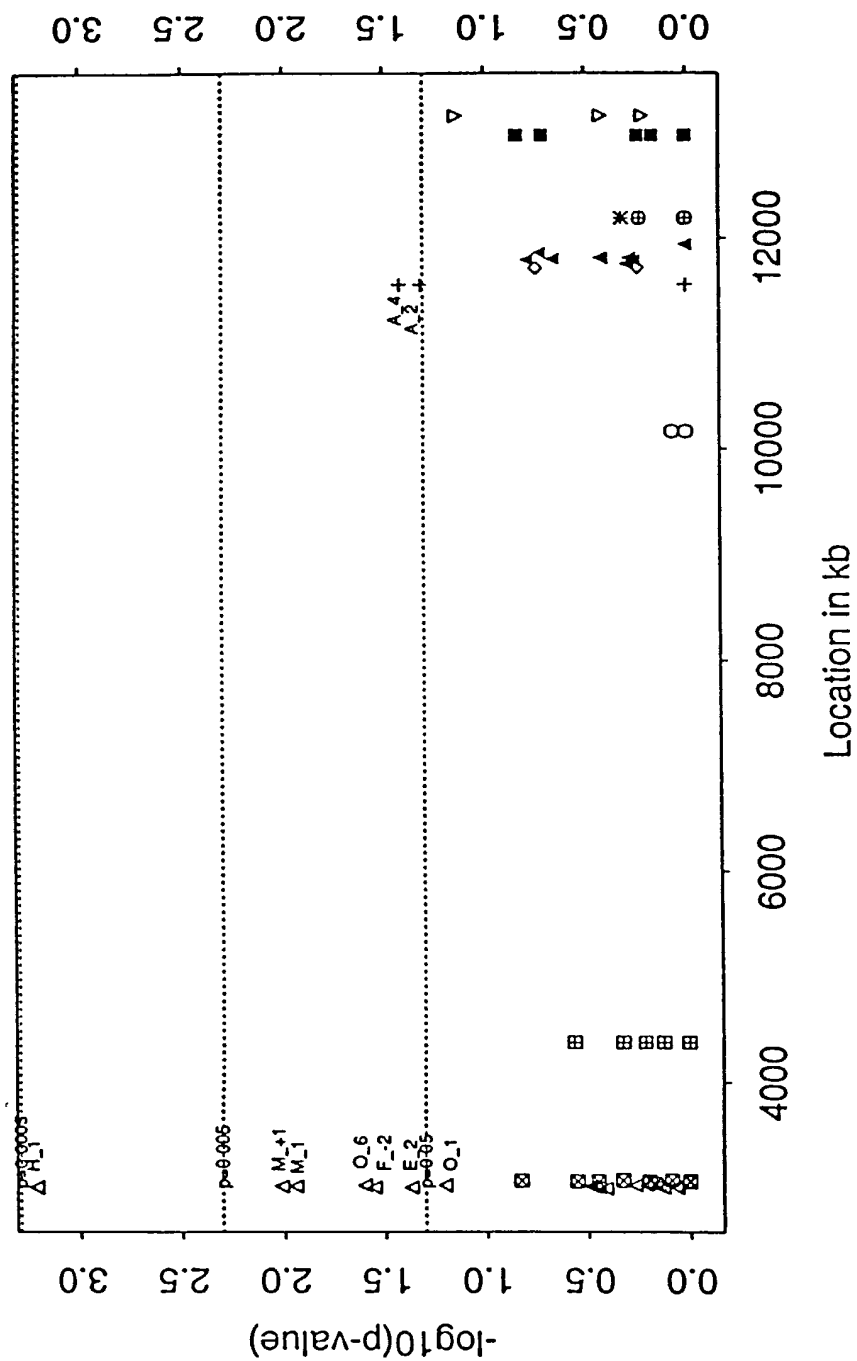


FIG. 17

FIG. 17 is a Manhattan plot showing the results of a genome-wide association study (GWAS) for the association between specific alleles and the case of Specific IgE and Asthma. The y-axis represents the negative logarithm of the p-value ($-\log_{10}(\text{p-value})$), and the x-axis represents the location in kilobases (kb). The plot shows several significant associations, with the most significant being at approximately 10,000 kb, where the p-value is less than 0.0005. The plot also shows the location of several genes, including gene 454, gene 436, gene 515, gene 570, gene 757, gene 698, gene 561, gene 581, gene 722, gene 702, and gene 214. The number 8 is also present near the 10,000 kb mark.

SU

JK

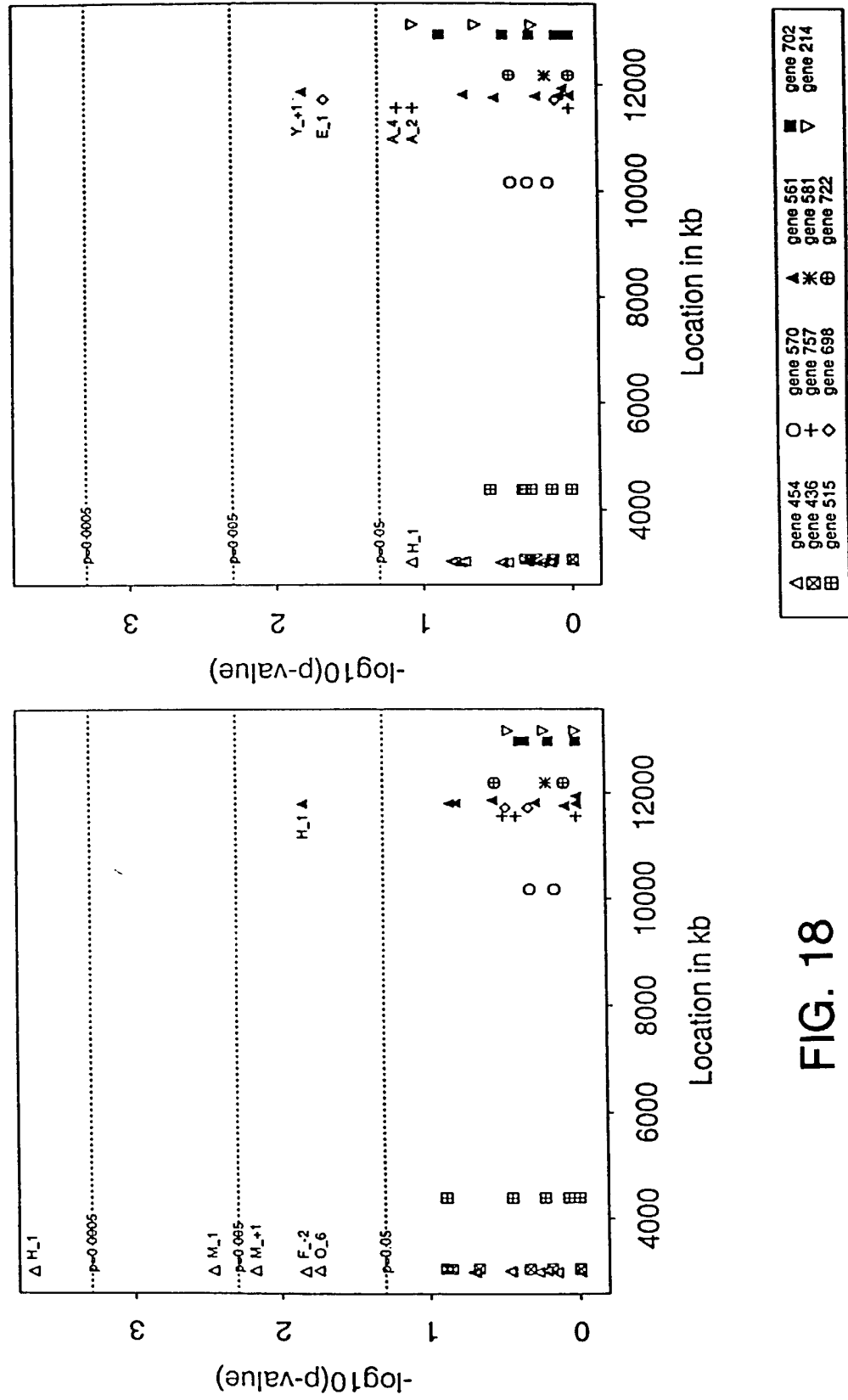


FIG. 18

Chr. 12 Case(Asthma)/Control: Haplotype

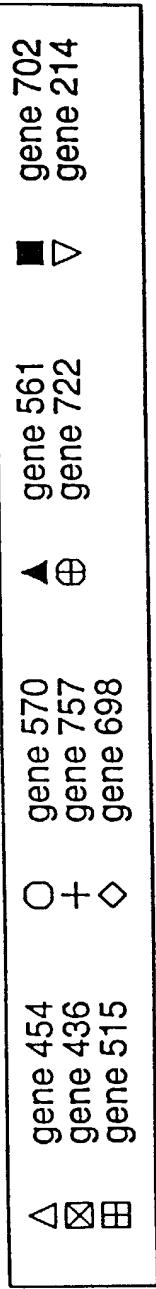
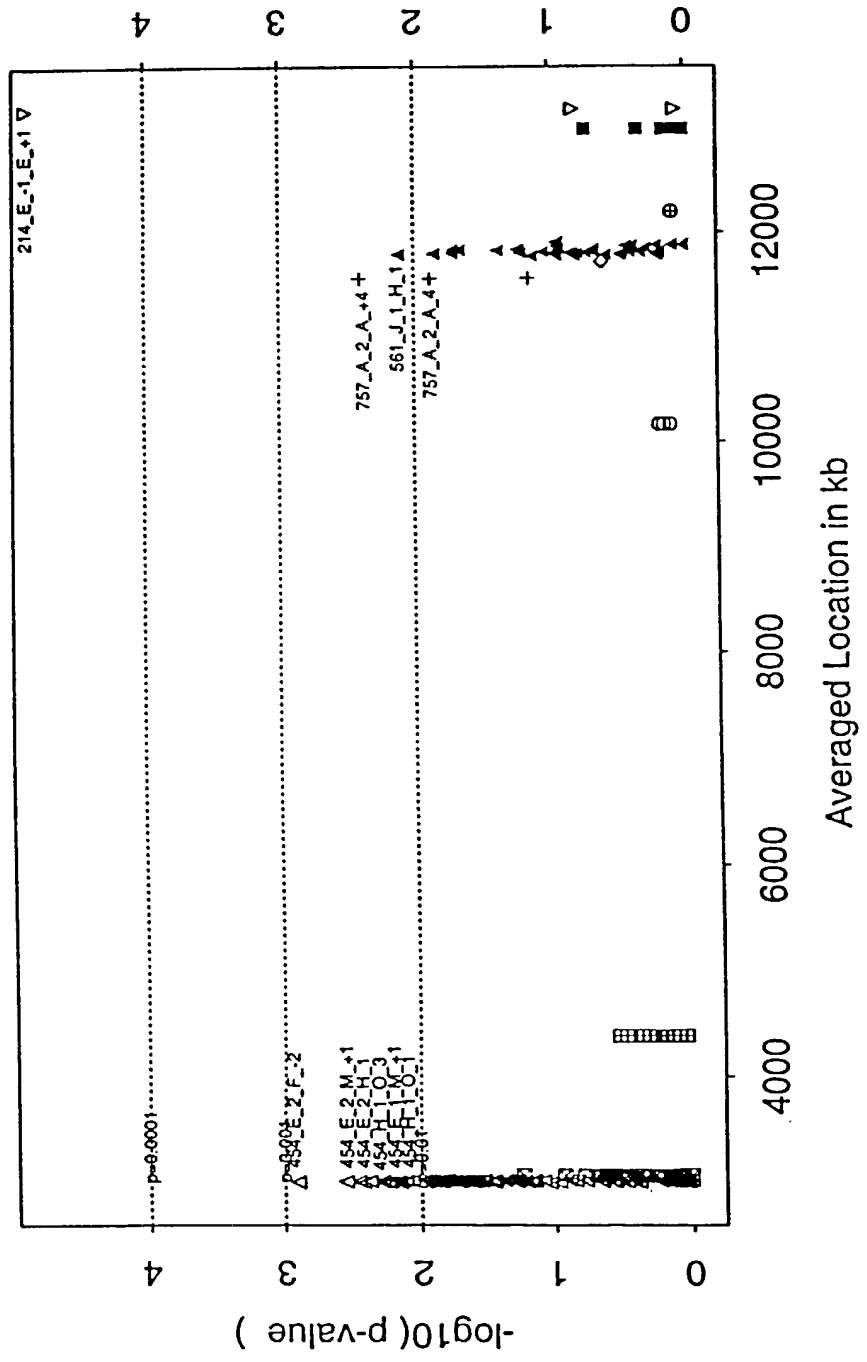


FIG. 19



Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype

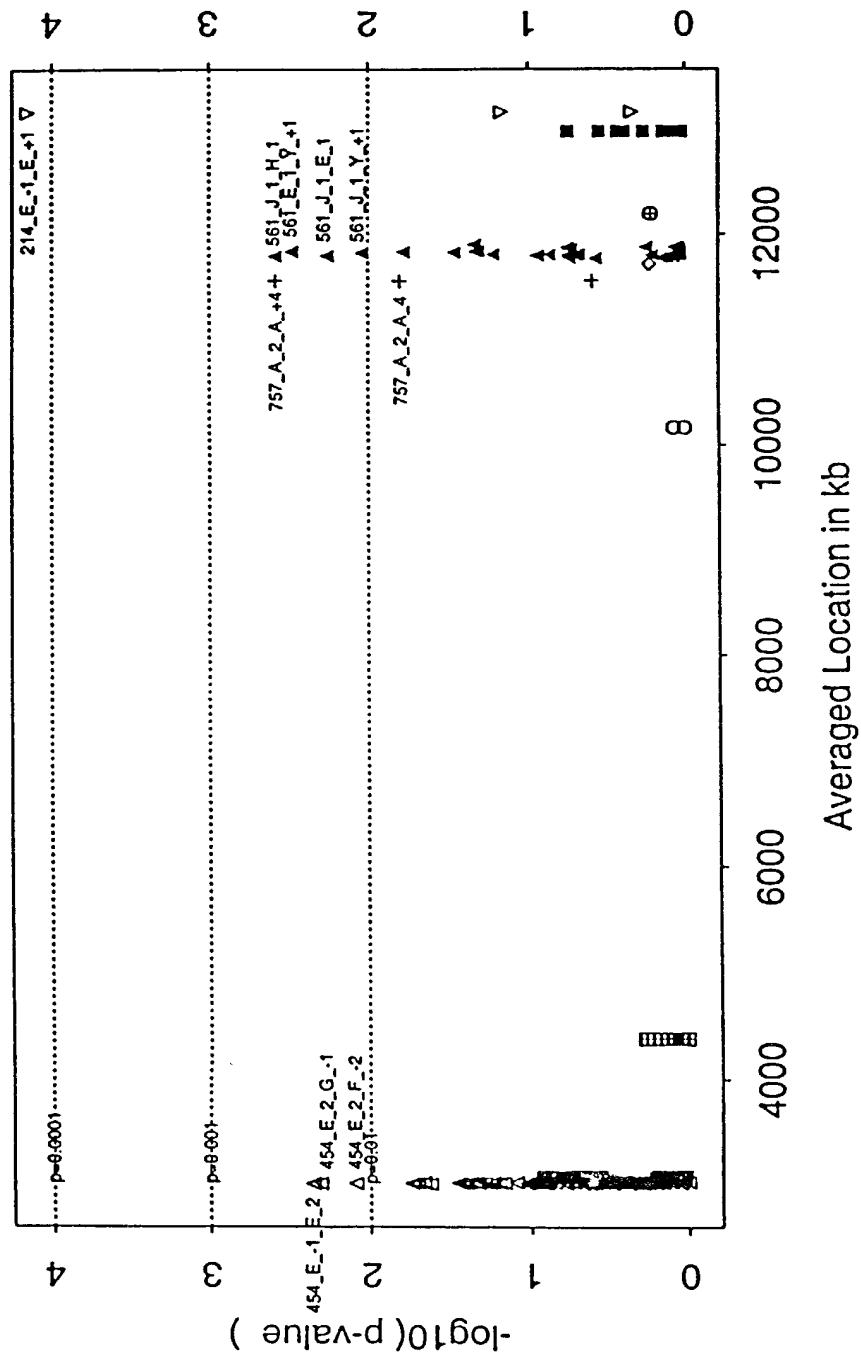


FIG. 21

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype

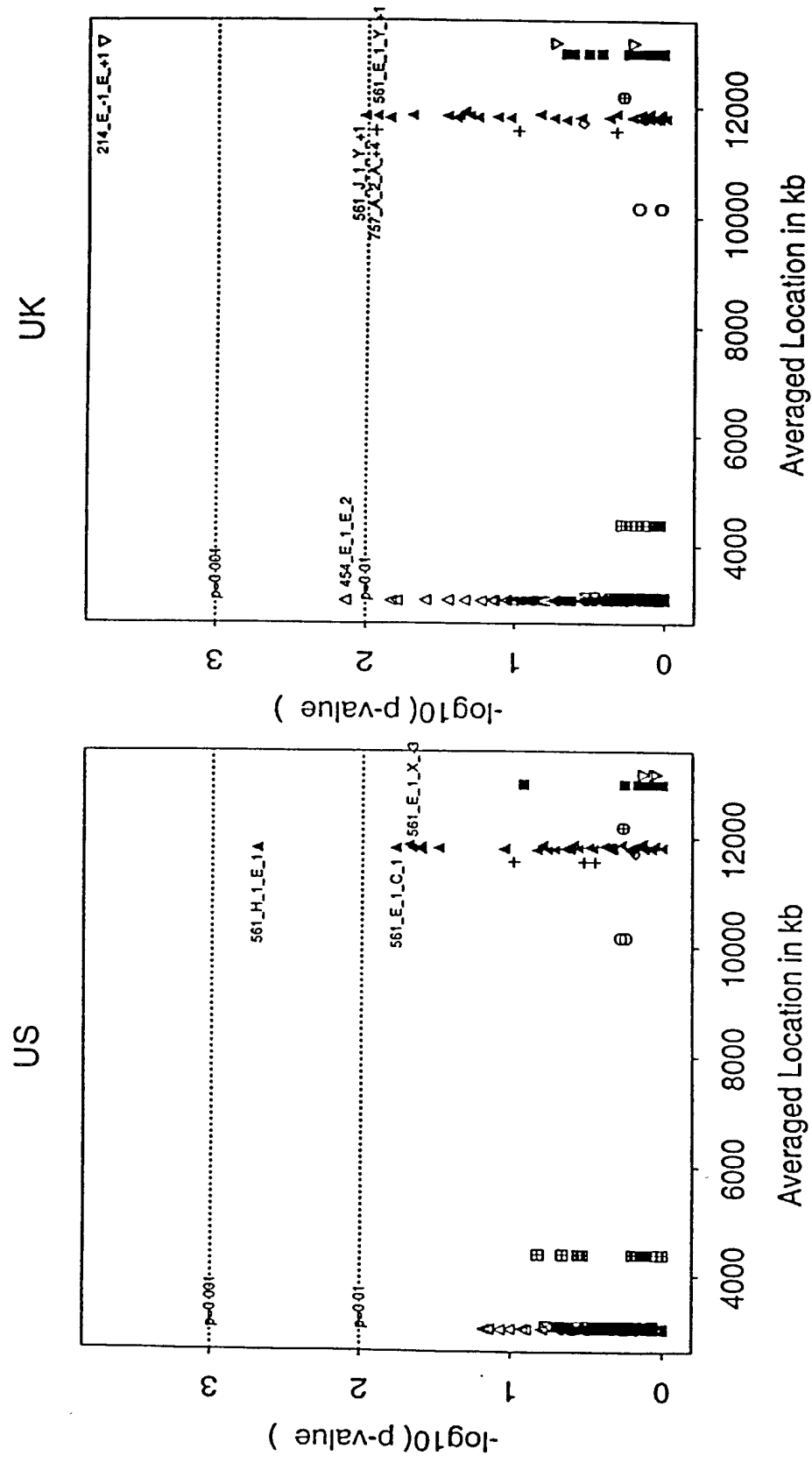


FIG. 22

Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

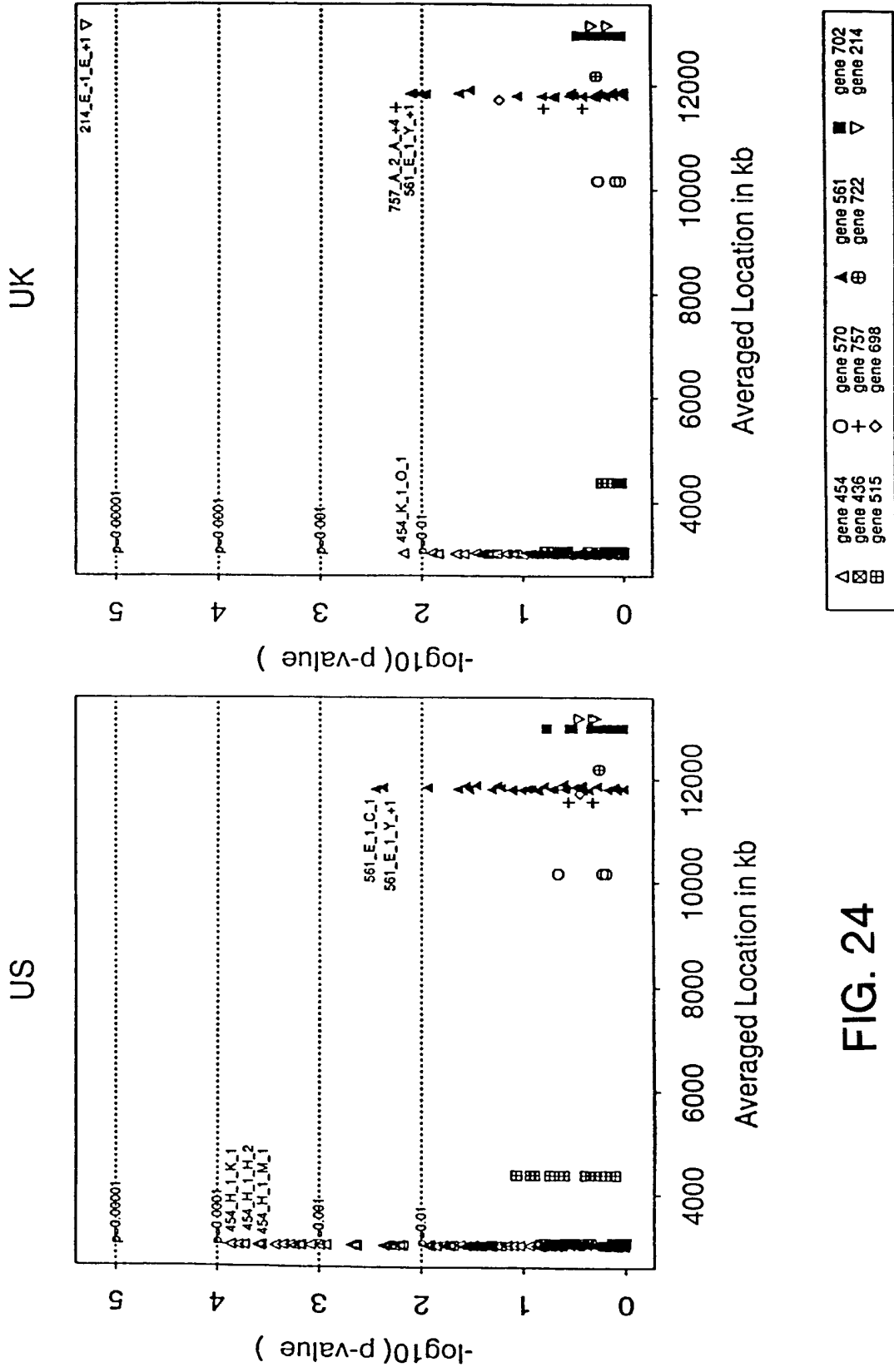


FIG. 24

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

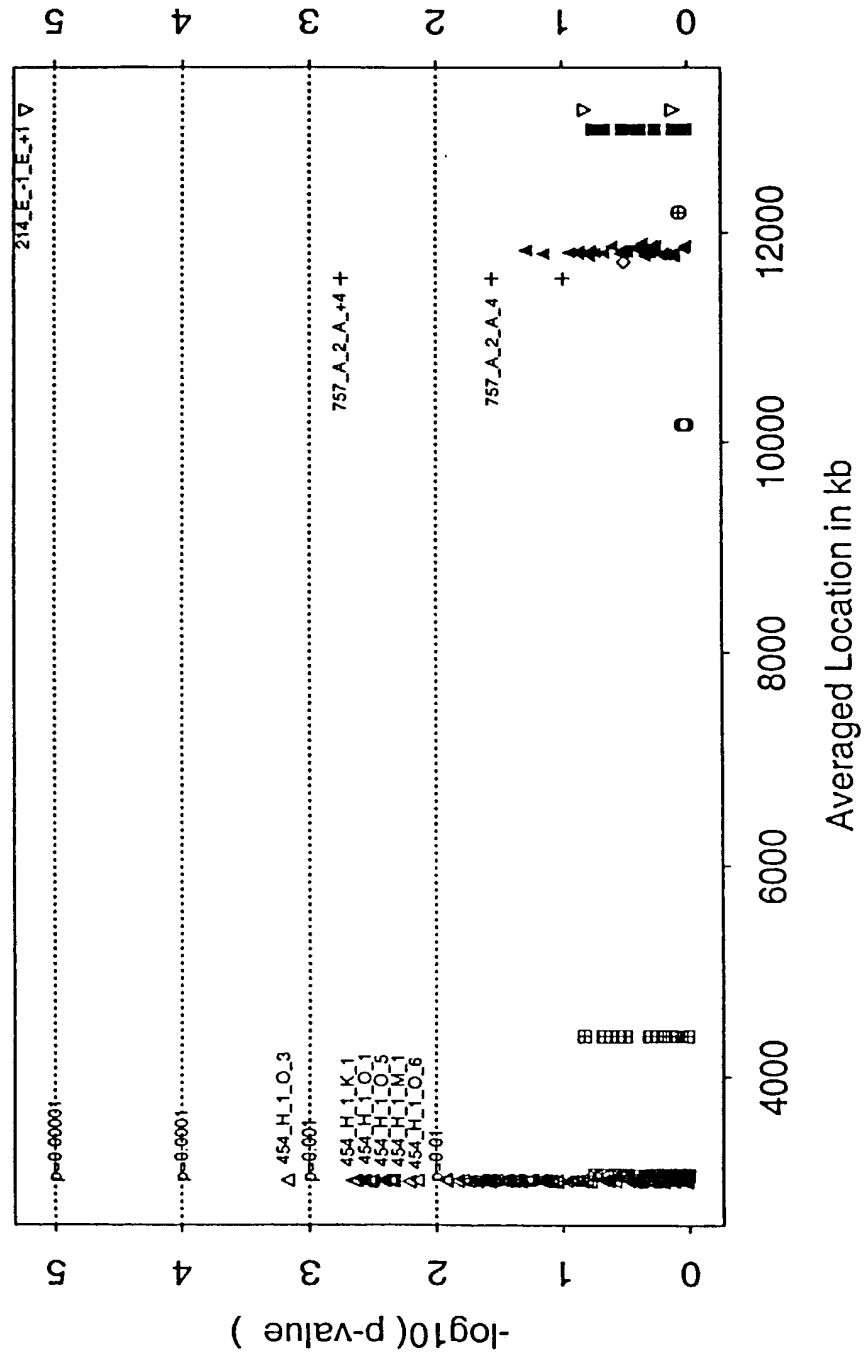
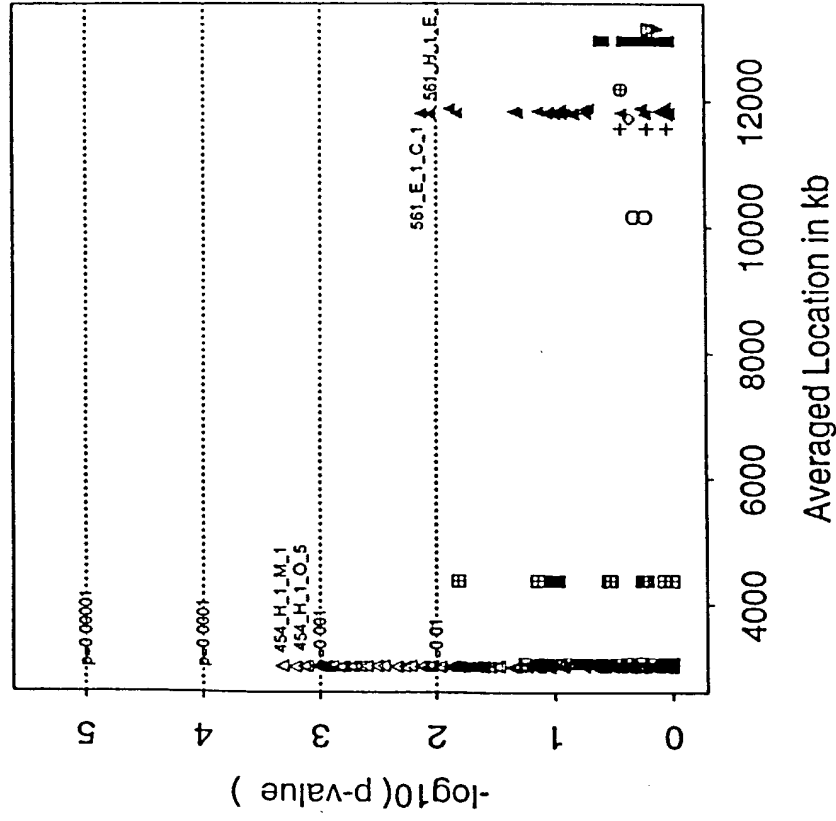


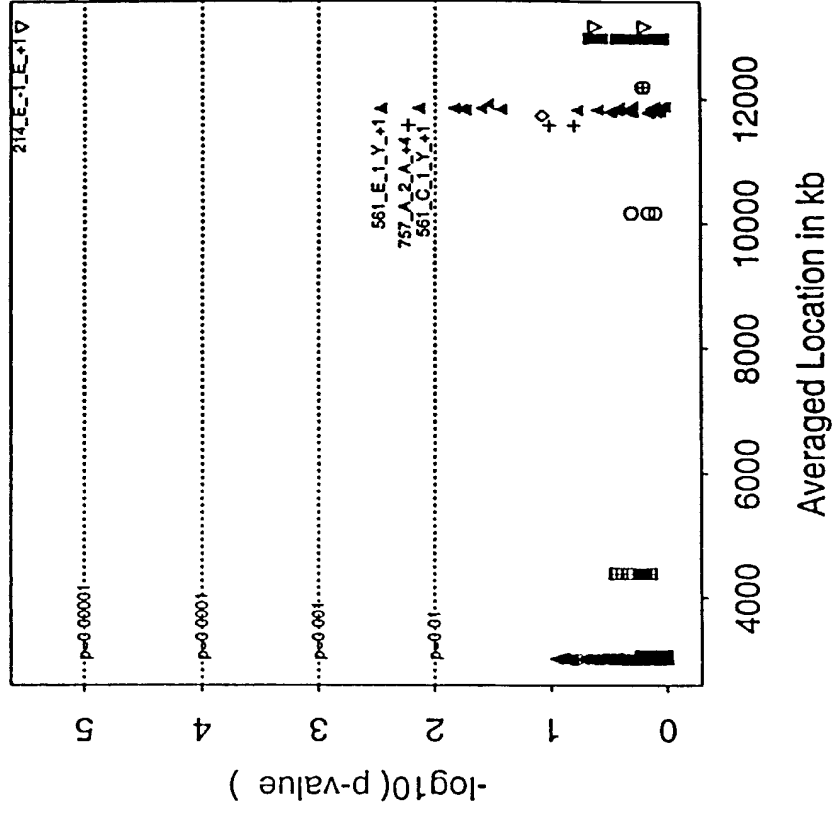
FIG. 25

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

US



UK



△	gene 454	○	gene 570	▲	gene 561	■	gene 702
⊠	gene 436	+	gene 757	⊕	gene 722	▽	gene 214
⊞	gene 515	◇	gene 698				

FIG. 26

FIG. 27A

610 630 650
 G C C C C C A G C A A G C C T T T C C C A C A G T T C A T G A A T G G C C T A G C C A C C T C C C T C G G C A A A G G T
 AlaProSerLysProPheProGlnPheMetAsnGlyLeuAlaThrSerLeuGlyLysGly

670 690 710
 C A G G A G A G C G C T A T T G G A G G C A G C T C T G C G A T C G G T G A A T A T A T C C G G C C C C T T C C G C A G
 GlnGluSerAlaIleGlyGlySerSerAlaIleGlyGluTyrIleArgProLeuProGln

730 750 770
 C C T G G T G A C A G G C C G G A G C C T C T G T C C G C C A A G C C C A C C T T C C T G T C G A G A T C C G G T A G C
 ProGlyAspArgProGluProLeuSerAlaLysProThrPheLeuSerArgSerGlySer

790 810 830
 G C A A G A T G C A G A T C T G A G T C A G A C A T G G A G A A T G A A C G G A A T T C C A A T A C C T C C A A G C A G
 AlaArgCysArgSerGluSerAspMetGluAsnGluArgAsnSerAsnThrSerLysGln

850 870 890
 A G A T A C T C G G G G A A G G T C C A C C T C T G T G T T G C C C G C T A T A G T T A C A A C C C C T T C G A T G G A
 ArgTyrSerGlyLysValHisLeuCysValAlaArgTyrSerTyrAsnProPheAspGly

910 930 950
 C C G A A C G A G A A C C C C G A A G C T G A G C T G C C C C T C A C G G C G G G A A A T A C C T C T A C G T C T A T
 ProAsnGluAsnProGluAlaGluLeuProLeuThrAlaGlyLysTyrLeuTyrValTyr

970 990 1010
 G G A G A C A T G G A T G A G G A T G G G T T C T A T G A A G G A G A G C T C C T C G A T G G C C A G A G G G T C T G
 GlyAspMetAspGluAspGlyPheTyrGluGlyGluLeuLeuAspGlyGlnArgGlyLeu

1030 1050 1070
 G T G C C C T C C A A C T T C G T G G A C T T T G T G C A G G A C A A C G A G T C G C G G T T G G C A A G C A C G C T G
 ValProSerAsnPheValAspPheValGlnAspAsnGluSerArgLeuAlaSerThrLeu

1090 1110 1130
 G G G A A C G A G C A G G A T C A G A A C T T C A T C A A C C A T T C C G G C A T C G G C C T G G A G G G A G A G C A C
 GlyAsnGluGlnAspGlnAsnPheIleAsnHisSerGlyIleGlyLeuGluGlyGluHis

1150 1170 1190
 A T C C T G G A C C T C C A C T C C C C A A C C C A C A T A G A T G C G G G C A T C A C C G A C A A C A G T G C C G G G

FIG. 27B

IleLeuAspLeuHisSerProThrHisIleAspAlaGlyIleThrAspAsnSerAlaGly

1210 1230 1250
ACCCTGGACGTGAACATCGACGACATCGGAGAAGACATCGTGCCTTACCCTAGAAAAATC
ThrLeuAspValAsnIleAspAspIleGlyGluAspIleValProTyrProArgLysIle

1270 1290 1310
ACCCTCATCAAACAACTCGCCAAAAGTGTTATTGTGGGCTGGGAGCCCCGGCGGTGCCA
ThrLeuIleLysGlnLeuAlaLysSerValIleValGlyTrpGluProProAlaValPro

1330 1350 1370
CCAGGATGGGGAACGGTGAGCAGCTACAACGTCCTGGTGGACAAGGAGACACGCATGAAC
ProGlyTrpGlyThrValSerSerTyrAsnValLeuValAspLysGluThrArgMetAsn

1390 1410 1430
CTCAGCTGGGGAGCAGAACTAAAGCCCTCATCGAGAAGCTCAACATGGCAGCCTGCACC
LeuThrLeuGlySerArgThrLysAlaLeuIleGluLysLeuAsnMetAlaAlaCysThr

1450 1470 1490
TACCGCATCTCCGTGCAGTGCCTCACCAGCAGGGGCAGCTCGGATGAGCTGCAGTGCACG
TyrArgIleSerValGlnCysValThrSerArgGlySerSerAspGluLeuGlnCysThr

1510 1530 1550
CTGCTGGTGGGCAAGGACGTGGTGGTGGCCCCCTCCACCTGCGGGTGGACAACATCACG
LeuLeuValGlyLysAspValValValAlaProSerHisLeuArgValAspAsnIleThr

1570 1590 1610
CAGATCTCCGCCCAGCTCTCCTGGCTACCCACCAACAGCAACTACAGCCACGTCATCTTC
GlnIleSerAlaGlnLeuSerTrpLeuProThrAsnSerAsnTyrSerHisValIlePhe

1630 1650 1670
CTCAACGAGGAGGAGTTCGACATCGTCAAGGCCGCCAGGTACAAGTACCAGTTCTTCAAT
LeuAsnGluGluGluPheAspIleValLysAlaAlaArgTyrLysTyrGlnPhePheAsn

1690 1710 1730
CTCAGGCCCCAACATGGCCTATAAGGTGAAGGTTCTGGCCAAACCCACACAGATGCCGTGG
LeuArgProAsnMetAlaTyrLysValLysValLeuAlaLysProHisGlnMetProTrp

FIG. 27C

1750 1770 1790
CAGCTCCCGCTGGAGCAAAGGGAGAAGAAGGAGGCCTTTGTGGAGTTCTCCACGTTGCCT
GlnLeuProLeuGluGlnArgGluLysLysGluAlaPheValGluPheSerThrLeuPro

1810 1830 1850
GCAGGACCCCCAGCACCCCCACAAGATGTTACCGTCCAGGCTGGGGTGACCCCCGCCACC
AlaGlyProProAlaProProGlnAspValThrValGlnAlaGlyValThrProAlaThr

1870 1890 1910
ATCCGGGTCTCCTGGAGACCACCTGTGCTGACGCCCACCGGGCTGTCCAATGGCGCAAAC
IleArgValSerTrpArgProProValLeuThrProThrGlyLeuSerAsnGlyAlaAsn

1930 1950 1970
GTTACCGGCTACGGCGTGTATGCCAAAGGGCAGAGGGTGGCTGAAGTCATCTTCCCCACG
ValThrGlyTyrGlyValTyrAlaLysGlyGlnArgValAlaGluValIlePheProThr

1990 2010 2030
GCAGACAGCACGGCCGTGGAGCTTGTGCGGCTGCGGAGCCTGGAGGCCAAGGGCGTGACC
AlaAspSerThrAlaValGluLeuValArgLeuArgSerLeuGluAlaLysGlyValThr

2050 2070 2090
GTGCGGACCCTCTCCGCCAGGGCGAGTCCGTGGACTCTGCAGTTGCTGCCGTTCCCCC
ValArgThrLeuSerAlaGlnGlyGluSerValAspSerAlaValAlaAlaValProPro

2110 2130 2150
GAGCTCCTGGTGCCTCCTACCCCCACCCGAGACCTGCACCCCAATCAAAGCCATTAGCA
GluLeuLeuValProProThrProHisProArgProAlaProGlnSerLysProLeuAla

2170 2190 2210
AGTTCTGGAGTCCCCGAAACCAAAGACGAGCACCTGGGTCCCCACGCCAGGATGGATGAG
SerSerGlyValProGluThrLysAspGluHisLeuGlyProHisAlaArgMetAspGlu

2230 2250 2270
GCCTGGGAGCAGAGCCGTGCACCTGGCCCTGTGCATGGGCACATGCTGGAGCCGCCCGTG
AlaTrpGluGlnSerArgAlaProGlyProValHisGlyHisMetLeuGluProProVal

2290 2310 2330
GGCCCCGGAAGGCGGTGCGCCTCACCCAGCCGCATCCTGCCGCAGCCACAGGGCACCCCG

FIG. 27D

GlyProGlyArgArgSerProSerProSerArgIleLeuProGlnProGlnGlyThrPro

2350 2370 2390
GTGTCCACCACCGTCGCCAAGGCCATGGCCCGGAGGCCGCGCAGAGGGTGGCCGAGAGC
ValSerThrThrValAlaLysAlaMetAlaArgGluAlaAlaGlnArgValAlaGluSer

2410 2430 2450
AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAAGCAGCGGGGGCAGTACGCCGCC
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

2470 2490 2510
TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGCGCCTCGGTGGAC
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

2530 2550 2570
GACTTCCTGAAAGGCTCTGAACTTGGCAAGCAGCCGCACTGTTGCCATGGAGACGAGTAC
AspPheLeuLysGlySerGluLeuGlyLysGlnProHisCysCysHisGlyAspGluTyr

2590 2610 2630
CACACAGAGAGCAGCCGGGGGTCTGACCTCTCAGACATCATGGAGGAGGACGAGGAGGAG
HisThrGluSerSerArgGlySerAspLeuSerAspIleMetGluGluAspGluGluGlu

2650 2670 2690
CTGTATTCTGAAATGCAGCTGGAAGATGGGGGAAGGAGGCGGCCAGCGGCACGTCCCAC
LeuTyrSerGluMetGlnLeuGluAspGlyGlyArgArgArgProSerGlyThrSerHis

2710 2730 2750
AATGCCCTCAAGATTTTAGGGAACCCAGCCTCTGCAGGACGGGTGGATCAGATGGGCCCGG
AsnAlaLeuLysIleLeuGlyAsnProAlaSerAlaGlyArgValAspHisMetGlyArg

2770 2790 2810
AGGTTTCCCCGTGGCAGCGCTGGTCCTCAGAGGTCCCGGCCCGTGACAGTCCCATCCATC
ArgPheProArgGlySerAlaGlyProGlnArgSerArgProValThrValProSerIle

2830 2850 2870
GACGATTACGGGCGAGACCGCCTTTCTCCAGACTTCTATGAAGAGTCAGAACTGACCCT
AspAspTyrGlyArgAspArgLeuSerProAspPheTyrGluGluSerGluThrAspPro

FIG. 27E

2890 2910 2930
GGTGCCGAAGAGCTCCCGGCCGGATCTTGTGGCTCTCTTTGACTACGACCCGCTCACC
GlyAlaGluGluLeuProAlaArgIlePheValAlaLeuPheAspTyrAspProLeuThr

2950 2970 2990
ATGTCCCCAAACCCAGATGCTGCAGAGGAGGAGCTTCCCTTTAAAGAAGGCCAGATCATC
MetSerProAsnProAspAlaAlaGluGluGluLeuProPheLysGluGlyGlnIleIle

3010 3030 3050
AAGGTTTATGGTGATAAAGACGCTGATGGATTCTACCGTGGGGAAACCTGTGCCCGGCTT
LysValTyrGlyAspLysAspAlaAspGlyPheTyrArgGlyGluThrCysAlaArgLeu

3070 3090 3110
GGCCTTATTCCCTTGTAACATGGTCTCTGAGATACAAGCAGATGATGAGGAGATGATGGAT
GlyLeuIleProCysAsnMetValSerGluIleGlnAlaAspAspGluGluMetMetAsp

3130 3150 3170
CAGCTTCTTAGACAGGGCTTTCTCCCTCTGAATACACCTGTGGAGAAAATAGAGAGAAGC
GlnLeuLeuArgGlnGlyPheLeuProLeuAsnThrProValGluLysIleGluArgSer

3190 3210 3230
AGGAGAAGTGGCAGGCGTCATTCCGGTATCGACGCGGAGAATGGTGGCCCTGTATGACTAC
ArgArgSerGlyArgArgHisSerValSerThrArgArgMetValAlaLeuTyrAspTyr

3250 3270 3290
GACCCAGAGAAAGCTCGCCCAACGTCGATGTCGAGGCCGAACCTACATTTTGCACAGGA
AspProArgGluSerSerProAsnValAspValGluAlaGluLeuThrPheCysThrGly

3310 3330 3350
GATATTATTACAGTTTTTGGTGAAATTGATGAAGATGGATTTTATTATGGGGAGCTGAAC
AspIleIleThrValPheGlyGluIleAspGluAspGlyPheTyrTyrGlyGluLeuAsn

3370 3390 3410
GGGCAGAAAGGCCTTGTGCCCTCAAACCTCTTGAAGAAGTGCCTGATGACGTAGAAGTC
GlyGlnLysGlyLeuValProSerAsnPheLeuGluGluValProAspAspValGluVal

3430 3450 3470
TATCTTTCTGATGCTCCATCCCACTACTCTCAAGATACGCCAATGCGCTCAAAGGCCAAAA

FIG. 27F

[illegible]

GA

FIG. 27G

4150 4170 4190
GAAGCACGCAGCTCAAATGATCACATTAGATGGAATAGATGGTATCTTCAGGTGTACTTT

4210 4230 4250
GGGATGCTTTACTAGGTGTTTTCCATTAGAATTAGACCTTGATTTTAAATCCAAGCAAGC

4270 4290 4310
TTGAAGCCCCTTGGCTTACAGCATTTCGCTGCTGAATACTAAACACTCACATGGCAAGAG

4330 4350 4370
TTGCTCTGGAGAGGTAGGGCCAGAGGAATGCTGCTGCACTGCCAACTCAGGCACATGCTT

4390 4410 4430
AGCTGTAAAGGGAAGCGAGGTGAAGTCGTCTGCAGCGTATTAGAGTAAAAGTCTACCCC

4450 4470 4490
TCTGAAGCACTATTAAGCGCTTAACGTATATTTAAATACTACCATGTGCTATCTACTGAG

4510 4530 4550
GAAGATTCAATGTTCAATTATTTGGAAATAATGCAAGCATCCACTAAGGGCCTTTAAGCTT

4570 4590 4610
TCTTTGATTATAATTAAGGTCATTTTAGTTTTTTTTTTTTCTTTCAACCAGTGCGCAT

4630 4650 4670
CTCCAATATTTCTATAGTATACCAACCACCCAGGAATGCACTTTAACAATATCAGGATT

4690 4710 4730
TTATATAACCAAATAGTTTCAAATACAACAAAATTCCTTTATGAACTTTGCTTTTTAA

4750 4770 4790
GACTACTGATGGGTACTCGGCCAACTTTACTATCAACCTAATTCAGATCATGTCTCCCC

FIG. 27H

FIG. 27I

GTTGCTCTCTGTCACCGCTGGCAGTCTGCTCTCATTGTCCAAGCTCTGATTGGGAGGTTG

5530

5550

5570

GGAGGGGACGTCTTATTAACAAACGGGGGCGCATAGCTATCACCTGTAGCTCCCTCCCTA

5590

5610

5630

CCTGTAATTCCAGTCTTTGTGCATTTGTCTGCTTAAAGGAATGATTTCAACCTT

5650

5670

5690

TCTCCCTTCTCAAAATGCTTGCCTCATAATGCATAACTTTCACTTTGACTCTGGTCTTGA

5710

5730

5750

AATTCCTAGTTTAATTCGCCTTGATGTTCTGCCTTATAAATGCACAATGATTTGTACTGT

5770

5790

5810

CTAATAAAAACAGTGTATACTTTGTATGTGTCGTGCATTTCAGTGGTCTTCATCCTGACAC

5830

5850

5870

AGTGGTTTCGAGATCAAGTTGTACAGGCTGTGCATTTTAAGATACTAGTTTCAGTCTTTCA

5890

5910

5930

AAGCCAGCCAGGCTACACACAGAAAATGTTTACTCAATCATTCAAAAAAGAGAAAAGGAG

5950

5970

5990

AGAAAGTAACCTTTGTTTGGTAAAGCACCAGTACTCCAACCTTCCAGAAAGCCGATTATCT

6010

6030

6050

TCATTGCTTTTAATGTTCTATTCTGTGGCATTATGGTTTTCTGTTACTTTTCGTTGTCAAAA

6070

6090

6110

TGCCATACCCAAATACACAGCAATGAATGGCACACAAGTAATCCACATAATGCATAAGCC

6130

6150

6170

ACACCAAAACCAGACTCAATTTAAATCTGCTCCAATGAGTCCATACCCATCTTCATCAT

FIG. 27J

FIG. 27K

10 30 50
GGTCCCCACGCCAGGATGGATGAGGCCTGGGAGCAGAAGCCTGTGCACCTGGCCCTGTGC
MetAspGluAlaTrpGluGlnLysProValHisLeuAlaLeuCys

70 90 110
ATGGGCACATGCTGGAGCCGCGCCGTGGGCCCGCATCCTGCCACAGCCACAGGGCAGCCC
MetGlyThrCysTrpSerArgProTrpAlaProHisProAlaThrAlaThrGlyHisPro

130 150 170
GGTGTCCACCACCGTCGCCAAGGCCATGGCCCGGGAGGCCGCGCAGAGGGTGGCGAGAGC
GlyValHisHisArgArgGlnGlyHisGlyProGlyGlyArgAlaGluGlyGlyGluSer

190 210 230
AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAAGCAGCGCGGGGCAGTACGCCGCC
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

250 270 290
TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGCGCCTCGGTGGAC
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

310 330 350
GACTTCCTGAAAGGCTCTGAACTTGGCAAGCAGGGAACTGAGGCCACAGAATTGAGAA
AspPheLeuLysGlySerGluLeuGlyLysGlnGlyAsnEnd

370 390 410
TTTTTGTCCATGATTACGCAGATGGTCTCCTAACAGAGCTGGAATTAGATTGAACCGAGG

430 450 470
CCTGAAGAAGACCTGTTTCCACGCCTTTCCCATGTGCCACGTTCTCCTCACCTATCCAG

490 510 530
GAGTGAATCATCACCTTCCTGCAATCTGCTCAGGTTACAAACCCGGAGGAAAGGCTGGA

550 570 590
GCACTTGTTCTCTGGGTGAAGGACCCATACCCCCACTGGTTTTTGAGATCGGCATTACAGC

FIG. 28A

610 630 650
GCTGTCTTATGGCAGCCMCAGCCCCAGGTGGCCCCAGAGCCCTTGACATGTGGCCACCTG

670 690 710
GGGCTGAGTGTGACTGAGGCCCTGAATTTTACTTCTATAAAATTAGTTCCAGATTAGTT

730 750 770
TACATTCCCTAATTAGTTTACATGTAAACAGCCACACGTGGCTGGTGGCCACCAGTGCTGA

790 810 830
CGCCCAGCTCTGGATGACCACACCTGCTACAAGAGATGACTTTTCTAGAGAAGAGTAGAA

850 870 890
ACACAGCGGCAGAAACACAGCTCTGCACTTCCGAGGGCCTCCCACTCCTTCTGATGAGAC

910 930 950
TGCAGAGGAAGTCTGTTTGGCCAAGCATGCTATTAACACGTTTTCCTGCTTGTTTTGTTT

970 990 1010
TTTAACAGAGCAAACAGGTCTGTTTCTATTAAAATTTAAAAGCGTTAATATTTARCAGC

1030 1050 1070
ATTGTTTTATGTTGTATTTCATAACATAATAATATAACAATATATTAATTGTTAATATATA

1090 1110 1130
TTGTTAATAATATAATAATATAACATAAAATAAGTGATACTTATTTTCCATTTACAGTTG

1150 1170 1190
AGATATTTTCTTTAAAAGTAACGTAAATATTGATTCAATTCAAAGAATACATTCATTAA

1210 1230 1250
TCATACAGATGGCGTCTGGCTAGGTGACGCATCATGACAGTGGTAGGGAGTGACTGAAGT

1270 1290 1310

FIG. 28B

TGAGCTGGTGCACAGACTGCCAGTTTTACAAACCCGGAAGTGTTCCTGACCATCCGCTT

1330

1350

1370

CCCCATGCTGCCCCGCCCCGTCACATGAGCCCTTACCCCCTGGCGCTATCCCATCTGCTCC

1390

1410

1430

AAGACACCGATGTTCTAGTGGGTGGAAGCCTCCACTTTTAGTTGACTACGGTATCTCTAG

1450

1470

1490

CATTTCACACATAGTAGGTGCTCAATGAATGTTTGTCTGAATGAATGAATGAAAGAAGGGA

1510

1530

1550

GGCTGAGAGTAGCTGGGACATTTGCTCTGAAAAAATCACCTCCATTCTCCCAATATTACA

1570

1590

1610

AAAGCATTTTCATTAAGTCCACAATGAAAAATGCTCACTGTACCAATAAATAATATCTTT

1630

1650

AGTTATCTATTTTTAAAGTAAAAAAAACCTCGTGCCGAAGTC

FIG. 28C